

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:07:45 ; Search time 14.883 Seconds
(without alignments)
261.554 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGNWTFLLSLGTAHVSE.....RGANWFDWGGCTITLVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues
Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:*

- 1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB pep:*
- 2: /cgn2_6/prodata/1/pubppa/US06_NEW_PUB pep:*
- 3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB pep:*
- 4: /cgn2_6/prodata/1/pubppa/PCT_NEW_PUB pep:*
- 5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB pep:*
- 6: /cgn2_6/prodata/1/pubppa/US10_NEW_PUB pep:*
- 7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB pep:*
- 8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	571	77.5	115	7	US-11-165-023-16
2	569.5	77.3	117	7	US-11-074-373-39
3	558	75.7	115	7	US-11-165-023-31
4	555	75.3	115	7	US-11-165-023-32
5	541.5	73.5	592	6	US-10-016-686-4
6	541	73.4	138	7	US-11-125-837-22
7	539.5	73.2	139	6	US-10-504-389A-28
8	526	71.4	140	7	US-11-193-512-27
9	502	68.1	140	7	US-11-193-512-63
10	501	68.0	136	7	US-11-250-411-88
11	499.5	67.8	153	7	US-11-126-798-4
12	498.5	67.6	133	6	US-10-932-334-52
13	498.5	67.6	293	7	US-11-116-939-10
14	498.5	67.6	412	7	US-11-116-939-12
15	498.5	67.6	824	7	US-11-116-939-11
16	494	67.0	142	7	US-11-170-453-7
17	491	66.6	130	7	US-11-188-187A-3
18	490	66.5	140	7	US-11-193-512-74
19	488.5	66.3	488	6	US-10-016-686-3
20	487	66.1	462	7	US-11-177-648-9
21	485.5	65.9	138	7	US-11-089-872-3
22	485	65.8	140	7	US-11-183-205-62
23	483.5	65.6	243	6	US-10-016-686-1
24	482	65.4	136	7	US-11-250-411-91
25	480.5	65.2	114	7	US-11-102-743-7

26	480	65.1	119	7	US-11-097-812-71	Sequence 71, Appl
27	480	65.1	119	7	US-11-097-812-72	Sequence 72, Appl
28	480	65.1	119	7	US-11-097-812-73	Sequence 73, Appl
29	480	65.1	119	7	US-11-097-812-74	Sequence 74, Appl
30	480	65.1	119	7	US-11-097-812-76	Sequence 76, Appl
31	480	65.1	119	7	US-11-097-812-81	Sequence 81, Appl
32	480	65.1	136	7	US-11-250-411-95	Sequence 95, Appl
33	479	65.0	120	7	US-11-097-812-144	Sequence 144, App
34	478	64.9	140	7	US-11-193-512-78	Sequence 78, Appl
35	477	64.7	462	7	US-11-177-648-30	Sequence 30, Appl
36	476.5	64.7	120	7	US-11-037-199-5	Sequence 5, Appl1
37	474.5	64.4	130	7	US-11-179-820-6	Sequence 6, Appl1
38	473	64.2	119	7	US-11-097-812-63	Sequence 63, Appl1
39	473	64.2	119	7	US-11-097-812-64	Sequence 64, Appl1
40	473	64.2	119	7	US-11-097-812-65	Sequence 65, Appl1
41	473	64.2	119	7	US-11-097-812-70	Sequence 70, Appl1
42	473	64.2	119	7	US-11-097-812-75	Sequence 81, Appl1
43	473	64.2	119	7	US-11-097-812-77	Sequence 77, Appl1
44	473	64.2	119	7	US-11-097-812-80	Sequence 80, Appl1
45	473	64.2	119	7	US-11-097-812-206	Sequence 206, App

ALIGNMENTS

RESULT 1
US-11-165-023-16
Sequence 16, Application US/11165023
GENERAL INFORMATION:
Publication No. US20060019342A1
APPLICANT: DaiI'Acqua, William
APPLICANT: Wu, Heiren
APPLICANT: Dameshroder, Melissa
TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
FILE REFERENCE: A6700US
CURRENT APPLICATION NUMBER: US/11/165,023
CURRENT FILING DATE: 2005-06-24
PRIOR APPLICATION NUMBER: US 60/583,184
PRIOR FILING DATE: 2004-06-25
PRIOR APPLICATION NUMBER: US 60/624,153
PRIOR FILING DATE: 2004-11-02
NUMBER OF SEQ ID NOS: 32
SOFTWARE: PatentIn version 3.3
SEQ ID NO 16
LENGTH: 115
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-16
Query Match 77.5%; Score 571; DB 7; Length 115;
Best Local Similarity 92.3%; Pred. No. 1e-39; 4; Indels 2; Gaps 1;
Matches 108; Conservative 3; Mismatches 4; Indels 2; Gaps 1;
QY 20 EVQLQSGPELVKGTASVKISCKASGYSTGYIMHWKQSHGKSLMIGISYNGATSY 79
DB 1 EVQLQSGPELVKGTASVKISCKASGYSTGYIMHWKQSHGKSLMIGISYNGATSY 60
QY 80 NQKFKKATFTVDTSSITMGNLSITSDSAVYRCAGANWFDWGGCTITLVSS 136
DB 61 NQKFKKATFTVDTSSITMGNLSITSDSAVYRCAGANWFDWGGCTITLVSS 115
RESULT 2
US-11-074-373-39
Sequence 39, Application US/11074373
GENERAL INFORMATION:
Publication No. US20060024302A1
APPLICANT: Achen et al.
TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBOD
TITLE OF INVENTION: AND METHODS OF USING SAME

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FILE REFERENCE: 28967/39969A
; CURRENT APPLICATION NUMBER: US/11/074,373
; CURRENT FILING DATE: 2005-03-07
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 39
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-074-373-39

Query Match
Best Local Similarity 77.3%; Score 569.5; DB 7; Length 137;
Matches 107; Conservative 13; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGWITWFLFLISGTAGVHSEVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSH 60
DB 1 MGNMGVFLFLISGTGVSHTIOLQSGPDLVKGASVKSCKASGYSFTGYMHWKQSH 60
61 GKSLWIGYISCVNGATSNOKFKGATFTVDTSSSTAYMWFNSLTSEDSAVYYCAR 120
DB 61 GKSLWIGYIDPFGDITVNOFKGKATLTVDKSSSTAFMHLNLTSEDSAVYYCAR 120
121 W-VEVDYWGQGTTLTVSS 136
DB 121 YGGMIDYWGQGTSTVSS 137

RESULT 3
US-11-165-023-31
; Sequence 31, Application US/11165023
; Publication No. US20060019342A1
; GENERAL INFORMATION:
; APPLICANT: Dai11,Acqua, William
; APPLICANT: Wu, Herren
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
; TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
; FILE REFERENCE: AE700US
; CURRENT APPLICATION NUMBER: US/11/165,023
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,184
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/624,153
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-31

Query Match
Best Local Similarity 75.7%; Score 558; DB 7; Length 115;
Matches 106; Conservative 3; Mismatches 6; Indels 2; Gaps 1;

QY 20 EVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSHGKSLWIGYISCVNGATSY 79
DB 1 EVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSHGKSLWIGYISCVNGATSY 60
80 NQFKGKATFTVDTSSSTAYMWFNSLTSEDSAVYYCARGANWVFDYWGQGTTLTVSS 136
DB 61 ADFKFKATFTVDTSSSTAYMWFNSLTSEDSAVYYCAR--SHAMDYWGQGTSTVSS 115

RESULT 4
US-11-165-023-32
; Sequence 32, Application US/11165023
; Publication No. US20060019342A1
; GENERAL INFORMATION:
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APPLICANT: Dai11,Acqua, William
; APPLICANT: Wu, Herren
; APPLICANT: Damschroder, Melissa
; TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAMMALIAN
; TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
; FILE REFERENCE: AE700US
; CURRENT APPLICATION NUMBER: US/11/165,023
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: US 60/583,184
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/624,153
; PRIOR FILING DATE: 2004-11-02
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 32
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: recombinant antibody variable region
US-11-165-023-32

Query Match
Best Local Similarity 75.3%; Score 555; DB 7; Length 115;
Matches 105; Conservative 4; Mismatches 6; Indels 2; Gaps 1;

QY 20 EVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSHGKSLWIGYISCVNGATSY 79
DB 1 EVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSHGKSLWIGYISCVNGATSY 60
80 NQFKGKATFTVDTSSSTAYMWFNSLTSEDSAVYYCARGANWVFDYWGQGTTLTVSS 136
DB 61 ADFKFKATFTVDTSSSTAYMWFNSLTSEDSAVYYCAR--SHAMDYWGQGTSTVSS 115

RESULT 5
US-10-016-686-4
; Sequence 4, Application US/10016686
; Publication No. US20060014222A1
; GENERAL INFORMATION:
; APPLICANT: Oxford Biomedica (UK) Limited
; APPLICANT: Kingeman, Alan
; APPLICANT: Kingeman, Susan Mary
; APPLICANT: Bebbington, Christopher Robert
; APPLICANT: Carol, Miles William
; APPLICANT: Ellard, Fiona Margaret
; APPLICANT: Myers, Kevin Alan
; TITLE OF INVENTION: Antibodies
; FILE REFERENCE: 674523-2012
; CURRENT APPLICATION NUMBER: US/10/016,686
; CURRENT FILING DATE: 2002-11-02
; PRIOR APPLICATION NUMBER: PCT/GB00/04317
; PRIOR FILING DATE: 2000-11-13
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: deduced amino acid sequence for the Ig-574 fusion protein
US-10-016-686-4

Query Match
Best Local Similarity 73.5%; Score 541.5; DB 6; Length 592;
Matches 105; Conservative 9; Mismatches 22; Indels 3; Gaps 1;

QY 1 MGWITWFLFLISGTAGVHSEVLOQSGPELVKTGASVKISCKASGYSFTGYMHWKQSH 60
DB 1 MGNMGVFLFLISGTAGVHSEVLOQSGPDLVKGASVKSCKASGYSFTGYMHWKQSH 60
61 GKSLWIGYISCVNGATSNOKFKGATFTVDTSSSTAYMWFNSLTSEDSAVYYCARG-- 118
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 17:50:10 ; Search time 301.766 Seconds
(without alignments)
198.019 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGMIWIFLFLSGTAGVHSE.....RGANWVPDYGQGTTLTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	136	6	ABU08927 Mouse amy
2	640.5	86.9	137	8	ADS94331 Antibody
3	594.5	80.7	135	2	AAW60866 Variable
4	594.5	80.7	135	3	AAV80293 Igm chime
5	594.5	80.7	590	2	AAW31751 H chain s
6	594.5	80.7	590	3	AAW71888 Anti-huma
7	594.5	80.7	590	2	AAW12908 Anti-huma
8	593.5	80.5	135	2	AAW68548 Anti-CD33
9	593.5	80.5	135	4	AAW69682 Murine M1
10	593.5	80.5	135	8	AD047773 Mouse M19
11	590.5	80.1	135	2	AAW28669 p12-h2.3
12	585.5	79.4	139	8	ADW94335 Antibody
13	581	78.8	138	8	ADR73595 Anti-AR a
14	575.5	78.1	137	2	AAW05090 Heavy cha
15	575.5	78.1	467	6	AAE38408 Mouse vir
16	573.5	77.8	137	2	AAW03724 Anti-huma
17	571	77.5	115	9	AAE34944 Human ant
18	571	77.5	115	9	AEH17185 EPHA2 -spe
19	571	77.5	115	9	AEH42985 EPHA2 ant
20	567.5	77.0	152	8	ADU57084 3G4 antiB
21	567.5	77.0	159	8	ADJ57088 3G4-2BVA-
22	564	76.5	138	4	AAW69688 Murine CM
23	564	76.5	138	8	AD047789 Mouse CMV
24	562.5	76.3	133	8	AD000820 Antibody

25	562.5	76.3	133	8	AD043850 Heavy cha
26	562.5	76.3	133	8	AD043846 Heavy cha
27	562.5	76.3	133	9	AD208854 Mammalian
28	562	76.3	140	2	AAW06213 MAb Co-1
29	562	76.3	140	2	AAW85061 Mouse Co-
30	562	76.3	140	6	AAW58895 Mouse ant
31	562	76.3	438	5	AAE18372 Human pen
32	562	76.3	438	5	ABG76347 Portion o
33	562	76.3	456	5	AAE18370 Human pen
34	562	76.3	456	5	ABG76345 Mouse DAV
35	562	76.3	456	9	ABE96754 DAV-1 ant
36	562	76.3	493	5	AAE18379 Human N-t
37	562	76.3	493	5	ABG76354 Mouse DAV
38	562	76.3	510	5	AAE18378 Human N-t
39	562	76.3	510	5	ABG76353 Mouse DAV
40	562	76.3	597	5	AAE18377 Human N-t
41	562	76.3	597	5	ABG76352 Mouse DAV
42	562	76.3	613	5	AAE18380 Human N-t
43	562	76.3	613	5	ABG76355 Mouse DAV
44	557.5	75.6	215	3	AAU78254 Mouse ag9
45	557	75.6	132	2	AAW03183 Guy's 13

ALIGNMENTS

RESULT 1	
ABU08927	ABU08927 standard; protein; 136 AA.
XX	ID
XX	ABU08927;
AC	ABU08927;
XX	
DT	03-JUN-2003 (first entry)
XX	
DE	Mouse amyloid beta antibody heavy chain variable region.
XX	
XX	Mouse; antibody; beta-amyloid fibril inhibitor; Alzheimer's disease;
KW	GMI ganglioside-bound amyloid beta protein; amyloid beta protein;
KW	amyloid fibril formation inhibition; heavy chain; variable region.
XX	
XX	Mus musculus.
OS	
XX	
XX	Key
FT	Location/Qualifiers
FT	1..19
FT	/label= Signal_sequence
FT	20..136
FT	/note= "Mature GMI ganglioside-bound amyloid beta
FT	antibody heavy chain variable region."
FT	50..54
FT	/label= CDR1
FT	/note= "Complementarity determining region 1.
FT	Specifically claimed in claim 1"
FT	69..85
FT	/label= CDR2
FT	/note= "Complementarity determining region 2.
FT	Specifically claimed in claim 1"
FT	118..125
FT	/label= CDR3
FT	/note= "Complementarity determining region 3.
FT	Specifically claimed in claim 1"
XX	
XX	MO2003014162-A1.
XX	
XX	20-FEB-2003.
XX	
XX	01-AUG-2002; 2002MO-JP007874.
XX	
XX	03-AUG-2001; 2001JP-00235700.
XX	
XX	(MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX	(NICH-) JAPAN CHUBU NAT HOSPITAL.
XX	(YANA/) YANAGISAWA K.

PI Yanagisawa K, Shibata M;
 XX WPI; 2003-268182/26.
 DR N-PSDB; ABX93688.
 XX Antibodies recognizing GM1 ganglioside-bound amyloid beta-protein and
 PT encoded DNAs, useful in diagnosing, preventing or treating Alzheimer's
 XX disease by inhibiting early-stage beta-amyloid fibril formation.
 XX
 PS Claim 4; Fig 1; 60pp; Japanese.
 CC The invention relates to four antibodies recognising GM1 ganglioside-
 CC bound amyloid beta protein and having inhibitory activity on the
 CC formation of amyloid fibril. The antibodies are useful in diagnosing,
 CC preventing or treating Alzheimer's disease by inhibiting early-stage beta
 CC -amyloid fibril formation. The antibody does not recognise soluble
 CC amyloid beta-protein, and thus drugs produced from the antibodies are
 CC efficacious in treating Alzheimer's disease. The present sequence
 CC represents the amino acid sequence of mouse GM1 ganglioside-bound amyloid
 CC beta antibody heavy chain variable region
 XX
 SQ Sequence 136 AA;
 Query Match 100.0%; Score 737; DB 6; Length 136;
 Best Local Similarity 100.0%; Pred. No. 4,2e-52;
 Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGWIMIFLPLISGTAGHSEVQLQSGPELVKTASVKISKAGSYSTGYMMVKQSH 60
 DB 1 MGWIMIFLPLISGTAGHSEVQLQSGPELVKTASVKISKAGSYSTGYMMVKQSH 60
 QY 61 GKSLEWIGYISCVNGATSYNCKEKGKATFTVDTSSSTAYVMOFNLSLSDSAVYYCARGAN 120
 DB 61 GKSLEWIGYISCVNGATSYNCKEKGKATFTVDTSSSTAYVMOFNLSLSDSAVYYCARGAN 120
 QY 121 WVPDYWGQGTTLTVSS 136
 DB 121 WVPDYWGQGTTLTVSS 136
 RESULT 2
 ADS94331
 ID ADS94331 standard; protein; 137 AA.
 AC ADS94331;
 XX
 DT 02-DEC-2004 (first entry)
 XX
 DE Antibody 368.1 heavy chain variable region (368.1H) SEQ ID NO:30.
 XX
 KW antibody; antigen-binding antibody fragment;
 KW cell-associated CA 125/0772P; monoclonal antibody; cytostatic;
 KW immunostimulant; mediator of lysis; tumour; cell proliferative disorder;
 KW cancer; cervical cancer; uterine cancer; breast cancer; lung cancer;
 XX ovarian cancer.
 XX
 OS Synthetic.
 XX
 PN MO2004035537-A2.
 PD 29-APR-2004.
 PF 15-OCT-2003; 2003WO-US032945.
 PR 16-OCT-2002; 2002US-0418828P.
 PR 10-JUL-2003; 2003US-0485986P.
 XX
 PA (EURO-) EUROCELTIQUE SA.
 PI Albane EF, Soltis DA;
 DR WPI; 2004-357171/33.
 DR N-PSDB; ADS94339.

XX
 PT Novel isolated antibody, or antigen-binding antibody fragment binding
 PT with cell-associated CA 125/0772P polypeptide relative to shed CA
 PT 125/0772 polypeptide, useful for ameliorating cervical or ovarian cancer.
 XX
 PS Claim 36; SEQ ID NO 30; 153pp; English.
 CC
 CC The present invention describes an isolated antibody, or an antigen-
 CC binding antibody fragment (I), that preferentially binds cell-associated
 CC CA 125/0772P polypeptide relative to shed CA 125/0772 polypeptide. Also
 CC described: (1) a monoclonal antibody (II) produced by hybridoma 4E7; (2)
 CC a monoclonal antibody that competes with binding of (II); (3) a hybridoma
 CC as deposited in (II); (4) an isolated nucleic acid molecule (III)
 CC comprising a nucleotide sequence that encodes a variable chain region of
 CC (I); (5) a pharmaceutical composition comprising an antibody or an
 CC antigen-binding antibody fragment that preferentially binds cell-
 CC associated CA 125/0772P polypeptide relative to shed CA 125/0772P
 CC polypeptide, and a carrier; (6) a pharmaceutical composition comprising a
 CC monoclonal antibody or an antigen-binding monoclonal antibody fragment
 CC that preferentially binds cell-associated CA 125/0772P polypeptide
 CC relative to shed CA 125/0772P polypeptide, and a carrier; (7) an article
 CC of manufacture (IV) comprising packaging material and a composition
 CC comprising an antibody, or an antigen-binding antibody fragment that
 CC preferentially binds cell-associated CA 125/0772P relative to shed CA
 CC 125/0772P, and a carrier contained within the packaging material, and
 CC composition in a form suitable for administration to a subject; (8) a
 CC fusion polypeptide (V) comprising an antibody, or an antigen-binding
 CC antibody fragment, which preferentially binds cell-associated CA
 CC 125/0772P relative to shed CA 125/0772P operably linked to a heterologous
 CC agent; (9) ameliorating (M1) a symptom of a CA 125/0772P-related disorder
 CC (10) a monoclonal antibody (VI) chosen from 325.1, 621.1, 633.1, 654.1,
 CC 725.1, 809, 7F10, 8A1, 8AC3, 15C9, 8E3, 8B5, 7G10, 16C7, 7C6, 7H1, 16H9,
 CC 7A11, 4E7, 117.1, 368.1, 446.1, 501.1, and 776.1 or its antigen-binding
 CC antibody fragment; (11) an antibody or antigen binding antibody fragment
 CC that competes with (VI); and (12) a pharmaceutical composition comprising
 CC (VI) and a carrier. (I) has cytostatic activity, and can be used as an
 CC immunostimulant and a mediator of lysis of positive tumour cell. (I) is
 CC useful for ameliorating a symptom of a CA 125/077P-related disorder which
 CC is a cell proliferative disorder such as cancer, cervical or uterine
 CC cancer, breast or lung cancer or ovarian cancer. (V) is useful
 CC diagnostically for monitoring the development or progression of cancer or
 CC tumour as part of clinical testing procedure. The present sequence
 CC represents an antibody heavy chain variable region amino acid sequence,
 CC which is used in the exemplification of the present invention.
 XX
 SQ Sequence 137 AA;
 Query Match 86.9%; Score 640.5; DB 8; Length 137;
 Best Local Similarity 87.6%; Pred. No. 2.8e-44;
 Matches 120; Conservative 8; Mismatches 8; Indels 1; Gaps 1;
 QY 1 MGWIMIFLPLISGTAGHSEVQLQSGPELVKTASVKISKAGSYSTGYMMVKQSH 60
 DB 1 MGWIMIFLPLISGTAGHSEVQLQSGPELVKTASVKISKAGSYSTGYMMVKQSL 60
 QY 61 GKSLEWIGYISCVNGATSYNCKEKGKATFTVDTSSSTAYVMOFNLSLSDSAVYYCAR GA 119
 DB 61 GKSLEWIGYISCVNGATSYNCKEKGKATFTVDTSSSTAYVMOFNLSLSDSAVYYCARBGD 120
 QY 120 WVPDYWGQGTTLTVSS 136
 DB 121 YSMDPFWGQGTSTVSS 137
 RESULT 3
 AAW60866
 ID AAW60866 standard; protein; 135 AA.
 AC AAW60866;
 XX
 DT 10-SEP-1998 (first entry)
 XX
 DE Variable region of an anti-Pas antibody heavy chain.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:00:46 ; Search time 25.1472 Seconds
(without alignments)
520.356 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGWIFLFLSLSTAGVHSE.....RGANWVFDYMGQTTLVSS 136

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR 80: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	596	80.9	140	2 T01407	Ig heavy chain (my
2	592.5	80.4	137	2 H32513	Ig heavy chain pre
3	583.5	79.2	139	2 A27609	Ig heavy chain pre
4	561.5	76.2	135	2 P60057	Ig heavy chain pre
5	558	75.7	138	2 PH0105	anti-digoxin trans
6	540.5	73.3	469	2 S37483	Ig gamma-2a chain
7	540	73.3	117	1 HVM58A	Ig heavy chain pre
8	532	72.2	140	2 PH1482	Ig heavy chain v r
9	527	71.5	138	2 S45249	Ig heavy chain pre
10	527	71.5	151	2 PL0011	Ig heavy chain pre
11	522	70.8	140	2 PH1489	Ig heavy chain v r
12	521	70.7	166	2 PL0012	Ig heavy chain pre
13	519	70.4	140	1 HVM5G7	Ig heavy chain pre
14	514.5	69.8	150	2 PNO444	Ig heavy chain v r
15	514	69.7	136	1 HVM5B1	Ig heavy chain pre
16	511.5	69.4	474	1 G2MS11	Ig gamma-2b chain
17	510	69.2	140	2 PH1488	Ig heavy chain v r
18	507	68.8	117	1 HVM54E	Ig heavy chain v r
19	505	68.5	117	1 HVM5J5	Ig heavy chain v r
20	505	68.5	135	2 PH1493	Ig heavy chain v r
21	505	68.5	140	2 PH1484	Ig heavy chain v r
22	504	68.4	135	2 PH1492	Ig heavy chain v r
23	501.5	68.0	112	2 S09957	Ig heavy chain v-D
24	501	68.0	138	2 S21810	Ig heavy chain v r
25	500	67.8	140	2 A26194	Ig heavy chain v r
26	499.5	67.8	139	1 PH1498	Ig heavy chain v r
27	498.5	67.6	119	2 P30502	Ig heavy chain pre
28	498.5	67.6	119	2 P30502	Ig heavy chain v r
29	495.5	67.2	139	2 P80024	Ig heavy chain pre

30	493	66.9	140	2 PH1486	Ig heavy chain v r
31	493	66.9	140	2 PH1483	Ig heavy chain v r
32	491	66.6	136	2 PL0208	Ig heavy chain pre
33	488.5	66.3	141	2 JL0076	Ig heavy chain pre
34	487.5	66.1	128	2 I37267	Ig heavy chain v r
35	481.5	65.3	120	2 A49982	Ig heavy chain v r
36	480.5	65.2	133	2 PC1155	Ig heavy chain pre
37	480.5	65.2	122	2 PH0887	Ig heavy chain v r
38	479.5	65.1	118	1 HVM538	Ig heavy chain v r
39	479	65.0	135	2 PH1494	Ig heavy chain v r
40	478	64.9	138	2 B32513	Ig heavy chain pre
41	475	64.5	118	2 PL0200	Ig heavy chain pre
42	474.5	64.4	141	2 A39276	Ig heavy chain pre
43	473.5	64.2	137	1 G2MS43	Ig heavy chain pre
44	472	64.0	246	2 S38950	Ig gamma chain - m
45	472	64.0	446	2 S40295	Ig gamma-2a chain

ALIGNMENTS

RESULT 1
T01407
Ig heavy chain (myeloma M104E) - mouse (fragment)
C/Species: Mus sp. (mouse)
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000
C/Accession: T01407
R/Takahashi, S.; Matsura, Y.; Taniguchi, T.; Tamura, H.; Bitch, S.; Onishi, S.; Yamamoto
Microbiol. Immunol. 36, 855-863, 1992
A/Title: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and
A/Reference number: 214317; MUID:3116638; PMID:1474935
A/Accession: T01407
A/Status: translated from GB/EMBL/DBD
A/Molecule type: mRNA
A/Residues: 1-140 <TRK>
A/Cross-references: UNIPARC:UPI000011B29E; EMBL:S51851; NID:9262657
C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 80.9%; Score 596; DB 2; Length 140;
Best Local Similarity 83.8%; Pred. No. 1.3e-43;
Matches 114; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

Qy 1 MGWIFLFLSLSTAGVHSEVQLQSGPELVKTSASVKISCKASGYSTGYMMVKQSH 60
Db 1 MGWIFLFLSLSTAGVHSEVQLQSGPELVKTSASVKISCKASGYSTGYMMVKQSH 60
Qy 61 GKSLEWIGYISCVGATSYNQKFKGKATFTVDISSTAYMQFNSLTSEDSAVYYCARGAN 120
Db 61 GKSLEWIGIDINPNNGTSYNQKFKGKATLTVDKSSSTRAYQNLNLTSEDSAVYYCARDYD 120
Qy 121 WFDYMGQTTLVSS 136
Db 121 WFDYMGAGTTLVSS 136

RESULT 2

H32513
Ig heavy chain precursor V region (BXM16) - mouse
C/Species: Mus musculus (house mouse)
C/Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C/Accession: H32513
R/Kotler, R.; Strohal, R.; Balderas, R.S.; Johnson, M.E.; Noonan, D.J.; Duchosal, M.A.;
J. Clin. Invest. 82, 852-860, 1988
A/Title: Immunoglobulin kappa 1 light chain variable region gene complex organization and
A/Reference number: A94689; MUID:88331394; PMID:3138286
A/Accession: H32513
A/Molecule type: DNA
A/Residues: 1-137 <KOP>
A/Cross-references: UNIPARC:UPI0000114D9A; GB:M20831; NID:9196949; PIDD:AAA38848.1; PIDD:
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotrimer; immunoglobulin
F/34-117/Domain: immunoglobulin homology <IMM>

Query Match 80.4%; Score 592.5; DB 2; Length 137;
 Best Local Similarity 84.2%; Pred. No. 2,5e-43;
 Matches 117; Conservative 6; Mismatches 11; Indels 5; Gaps 2;

QY 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 DB 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 QY 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR-- 117
 DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 120

QY 118 GANWVFDYWGQGTTLTVSS 136
 DB 121 GSS--FDYWGQGTTLTVSS 137

RESULT 3
 A27609
 Ig heavy chain precursor V region (I29) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
 C:Accession: A27609
 R:Klein, D.; Neteupekt, J.; Sirlin, S.; Stavnezer, J.
 J. Immunol. 140, 1676-1684, 1988
 A>Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
 A:Reference number: A27609; MUID:88154467; PMID:3126234
 A:Accession: A27609
 A:Molecule type: DNA
 A:Residues: 1-139 <KLE>
 A:Cross-references: UNIPARC:UPI0000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; PI
 C:Genetics:
 A:Introns: 16/1
 C:Superfamily: Immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 79.2%; Score 583.5; DB 2; Length 139;
 Best Local Similarity 81.3%; Pred. No. 1.5e-42;
 Matches 113; Conservative 9; Mismatches 14; Indels 3; Gaps 1;

QY 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 DB 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 QY 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 120
 DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 120

QY 121 WVF--DYWGQGTTLTVSS 136
 DB 121 YSYAMDYWGQGTSTVSS 139

RESULT 4
 PS0057
 Ig heavy chain precursor V region (PAR) - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
 C:Accession: PS0057
 R:Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
 J. Biochem. 104, 337-343, 1988
 A>Title: Biased expression of variable region gene families of the immunoglobulin heavy
 A:Reference number: PS0057; MUID:89197817; PMID:2467902
 A:Accession: PS0057
 A:Molecule type: DNA
 A:Residues: 1-135 <YAO>
 A:Cross-references: UNIPARC:UPI000011B257; GB:ID00307; NID:g220448; PIDN:BA00213.1; PID
 A>Note: the authors encoding the codon AAG for residue 32 as Asn and GAC for 92 as Gly
 C:Comment: The gene encoding this protein was isolated from a hybridoma that produces an
 C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 76.2%; Score 561.5; DB 2; Length 135;
 Best Local Similarity 80.9%; Pred. No. 1e-40;
 Matches 110; Conservative 8; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 DB 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 QY 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 120
 DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 119

QY 121 WVF--DYWGQGTTLTVSS 136
 DB 120 YRGAVWGQGTTLTVSSA 135

RESULT 5
 PH0105
 anti-digoxin transfectoma antibody light chain V region precursor - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
 C:Accession: PH0105
 R:Neat, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seidman, J.G.
 Mol. Immunol. 27, 901-909, 1990
 A>Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain
 A:Reference number: PH0105; MUID:91015092; PMID:2120577
 A:Accession: PH0105
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-138 <NEA>
 A:Cross-references: UNIPARC:UPI0000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA3994
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 75.7%; Score 558; DB 2; Length 138;
 Best Local Similarity 76.1%; Pred. No. 2.1e-40;
 Matches 105; Conservative 12; Mismatches 19; Indels 2; Gaps 1;

QY 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 DB 1 MGVWIFFLISGTAAGHSEVQLQSGPELVKTAASVKISCKASGYSTGYMHWKQSH 60
 QY 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 118
 DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMGNLSLTSEDSAVYYCAR 120

QY 119 ANWVFDYWGQGTTLTVSS 136
 DB 121 NKWAMDYWGAGATVSS 138

RESULT 6
 S37483
 Ig gamma-2a chain - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C:Accession: S37483
 R:Ducancel, F.F.D.
 Submitted to the EMBL Data Library, February 1993
 A:Reference number: S37483
 A:Accession: S37483
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-469 <DUC>
 A:Cross-references: UNIPARC:UPI000002B47; EMBL:X70423; NID:g406252; PIDN:CAA49868.1; PI
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: immunoglobulin

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 17:50:40 ; Search time 151.396 Seconds

(without alignments)
633.780 Million cell updates/sec

Title: US-10-768-193-7

Perfect score: 737
Sequence: 1 MGMIIFLFLSLGTAGVHSE.....RGANVPDYWGQITLTVSS 136

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Uniprot 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	605	80.1	470	Q7TMK1_MOUSE	Q7tmk1 mus musculu
2	592	80.3	472	Q6PJA7_MOUSE	Q6pja7 mus musculu
3	586	79.5	483	Q4VAB6_MOUSE	Q4vab6 mus musculu
4	567.5	77.0	488	Q91WRI_MOUSE	Q91wri mus musculu
5	548	74.4	477	Q58B56_MOUSE	Q58b56 mus musculu
6	546	74.1	481	Q91WT1_MOUSE	Q91wt1 mus musculu
7	542.5	73.6	481	Q8VCU5_MOUSE	Q8vcu5 mus musculu
8	540	73.3	117	HV14_MOUSE	Hv14 mus musculu
9	539.5	73.2	465	Q6PJB2_MOUSE	Q6pjb2 mus musculu
10	539	73.1	118	Q5RX00_MOUSE	Q5rx00 mus musculu
11	519	70.4	140	HV02_MOUSE	Hv02 mus musculu
12	516.5	70.1	613	Q8VCX7_MOUSE	Q8vcx7 mus musculu
13	516	70.0	117	Q9QXFO_MOUSE	Q9qxfo mus musculu
14	514	69.7	134	Q65ZRE_MOUSE	Q65zre mus musculu
15	514	69.7	136	HV15_MOUSE	Hv15 mus musculu
16	510	69.2	468	Q56W99_MOUSE	Q56w99 mus musculu
17	509	69.1	168	Q8VDC9_MOUSE	Q8vdc9 mus musculu
18	507	68.8	117	HV13_MOUSE	Hv13 mus musculu
19	505	68.5	117	HV13_MOUSE	Hv13 mus musculu
20	502	68.1	475	Q5FVP3_RAT	Q5fvp3 rattus norv
21	501	68.0	117	Q9QX89_MOUSE	Q9qx89 mus musculu
22	499.5	67.8	139	HV07_MOUSE	Hv07 mus musculu
23	499	67.7	473	Q9DB14_MOUSE	Q9db14 mus musculu
24	496.5	67.4	590	Q4Y9V8_MOUSE	Q4y9v8 mus musculu
25	496.5	67.4	617	Q4KML5_MOUSE	Q4kml5 mus musculu
26	494.5	67.1	485	Q58B61_MOUSE	Q58b61 mus musculu
27	491.5	66.7	463	Q991C4_MOUSE	Q991c4 mus musculu
28	491	66.6	480	Q8K0Z4_MOUSE	Q8k0z4 mus musculu
29	488	66.2	464	Q6PFS9_MOUSE	Q6pfs9 mus musculu
30	488	66.2	614	Q7TMT6_MOUSE	Q7tmt6 mus musculu
31	485.5	65.9	482	Q8K172_MOUSE	Q8k172 mus musculu

32	484.5	65.7	591	Q4Q0W0_RAT	Q4q0w0 rattus norv
33	480	65.1	616	Q50AM7_MOUSE	Q50am7 mus musculu
34	479.5	65.1	118	HV51_MOUSE	Hv51 mus musculu
35	479.5	65.0	458	Q5BK05_RAT	Q5bk05 rattus norv
36	477.5	64.8	598	Q568Y0_RAT	Q568y0 rattus norv
37	475	64.5	458	Q5BJ22_RAT	Q5bj22 rattus norv
38	473.5	64.2	137	HV11_MOUSE	Hv11 mus musculu
39	473	64.2	483	Q52151_MOUSE	Q52151 mus musculu
40	470.5	63.8	487	Q55ZL2_MOUSE	Q55zl2 mus sp. fv
41	467	63.4	489	Q8VCX4_MOUSE	Q8vcx4 mus musculu
42	464	63.0	117	HV52_MOUSE	Hv52 mus musculu
43	463	62.8	120	Q920E8_MOUSE	Q920e8 mus musculu
44	461.5	62.6	488	Q8K0F2_MOUSE	Q8k0f2 mus musculu
45	458.5	62.2	486	Q5HZY6_MOUSE	Q5hzy6 mus musculu

ALIGNMENTS

RESULT 1
Q7TMK1_MOUSE
ID Q7TMK1_MOUSE PRELIMINARY; PRT; 470 AA.
AC Q7TMK1;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Hypothetical protein A1324046.
GN Name=A1324046;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZCH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnae.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stachenko M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McGowan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huijck S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Heltón E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
RA Schnerch A., Schein J.E., Jones S.J.W., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=CZCH II;
RC TISSUE=Mammary tumor metastasized to lung. MMTV-LTR/Mnt1 model.
RC Expression driven by an MMTV-LTR enhancer.;
RA Strausberg R.L.;
RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC055910; AAHS5910.1; -; mRNA.
DR HSSP; P01865; IKB5.
DR GO; GO:0003823; F:antigen binding; IEA.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.

DR EMBL; BC018535, AAH18535.1, -; mRNA.
DR HSSP; P01865, 1KB5.

RC STRAIN=FVB/N; TISSUE=

RN	[2]
RP	NUCLEOTIDE SEQUENCE.

RP	NUCLEOTIDE SEQUENCE.
RC	STRAIN=FVB/N; TISSUE=Colon;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:06:30 ; Search time 122.657 Seconds
(without alignments)
463.284 Million cell updates/sec

Title: US-10-768-193-7

Perfect score: 737

Sequence: 1 MGMIWIFLFLSLGTAGVHSE.....RGANVFDYWGQGTTLTVSS 136

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10b_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	737	100.0	136	4	US-10-768-193-7
2	640.5	86.9	137	5	US-10-687-035-30
3	601.5	81.6	137	4	US-10-462-062-153
4	601.5	81.6	137	4	US-10-462-062-154
5	593.5	80.5	135	4	US-10-389-155-60
6	593.5	80.5	135	4	US-10-389-417-60
7	593.5	80.5	135	4	US-10-452-357-69
8	593.5	80.5	135	5	US-10-837-904-27
9	585.5	78.4	139	5	US-10-687-035-34
10	581	78.8	138	4	US-10-774-076-9
11	575.5	78.1	467	5	US-10-500-696-2
12	571	77.5	115	5	US-10-994-129-21
13	571	77.5	115	6	US-11-004-795A-53
14	571	77.5	115	6	US-11-004-794A-53
15	567.5	77.0	152	4	US-10-642-120-2
16	567.5	77.0	152	4	US-10-642-060-2
17	567.5	77.0	152	4	US-10-642-122-2
18	567.5	77.0	152	4	US-10-642-059-2
19	567.5	77.0	152	4	US-10-642-124-2
20	567.5	77.0	152	4	US-10-621-269-2
21	567.5	77.0	152	4	US-10-620-850-2
22	567.5	77.0	152	4	US-10-642-118-2
23	567.5	77.0	152	4	US-10-642-119-2
24	567.5	77.0	152	4	US-10-642-117-2
25	567.5	77.0	152	5	US-10-642-099-2
26	567.5	77.0	152	5	US-10-642-064-2
27	567.5	77.0	152	5	US-10-642-116-2

28	567.5	77.0	152	5	US-10-642-100-2	Sequence 2, Appl1
29	567.5	77.0	152	5	US-10-642-058-2	Sequence 2, Appl1
30	567.5	77.0	152	5	US-10-642-121-2	Sequence 2, Appl1
31	567.5	77.0	152	5	US-10-642-065-2	Sequence 2, Appl1
32	567.5	77.0	152	5	US-10-642-071-2	Sequence 2, Appl1
33	564	76.5	138	4	US-10-389-155-72	Sequence 72, Appl1
34	564	76.5	138	4	US-10-389-417-72	Sequence 72, Appl1
35	564	76.5	138	4	US-10-452-357-85	Sequence 85, Appl1
36	562.5	76.3	133	5	US-10-810-881A-79	Sequence 79, Appl1
37	562	76.3	438	3	US-09-903-327A-6	Sequence 6, Appl1
38	562	76.3	456	3	US-09-903-327A-2	Sequence 2, Appl1
39	562	76.3	493	3	US-09-903-327A-13	Sequence 13, Appl1
40	562	76.3	510	3	US-09-903-327A-12	Sequence 12, Appl1
41	562	76.3	597	3	US-09-903-327A-11	Sequence 11, Appl1
42	562	76.3	613	3	US-09-903-327A-14	Sequence 14, Appl1
43	557	75.6	132	5	US-09-982-107-14	Sequence 14, Appl1
44	557	75.6	132	5	US-10-781-989-14	Sequence 14, Appl1
45	554.5	75.2	137	4	US-10-462-062-158	Sequence 158, App

ALIGNMENTS

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RESULT 1
US-10-768-193-7
; Sequence 7, Application US/10768193
; Publication No. US20040181042A1
; GENERAL INFORMATION:
; APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
; APPLICANT: The director of Chubu National Hospital
; APPLICANT: YANAGISAWA, Katsuhiko
; APPLICANT: SHIBATA, Masao
; TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
; TITLE OF INVENTION: amyloid b-protein and DNA encoding the antibody
; FILE REFERENCE: P0102402
; CURRENT APPLICATION NUMBER: US/10/768, 193
; PRIOR FILING DATE: 2004-02-02
; PRIOR APPLICATION NUMBER: JP P2001-235700
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: PCT/JP02/07874
; PRIOR FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 136
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-768-193-7
Query Match 100.0%; Score 737; DB 4; Length 136;
Best Local Similarity 100.0%; Pred. No. 2e-58;
Matches 136; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MGMIWIFLFLSLGTAGVHSEVOLQSGPELVKTGASVYISCKASGYSTGYMHWVKOSH 60
DB 1 MGMIWIFLFLSLGTAGVHSEVOLQSGPELVKTGASVYISCKASGYSTGYMHWVKOSH 60
QY 61 GKSLIEWIYICNGATSYNOKFKGKATFTVDTSSSTAYMOFNSLTSDSAVYYCARGN 120
DB 61 GKSLIEWIYICNGATSYNOKFKGKATFTVDTSSSTAYMOFNSLTSDSAVYYCARGN 120
QY 121 WVPDYWGQGTTLTVSS 136
DB 121 WVPDYWGQGTTLTVSS 136
RESULT 2
US-10-687-035-30
; Sequence 30, Application US/10687035
; Publication No. US20050064518A1
; GENERAL INFORMATION:
; APPLICANT: Albion, Earl F.
; APPLICANT: Solis, Daniel A.
```

TITLE OF INVENTION: ANTIBODIES THAT BIND CELL-ASSOCIATED
FILE REFERENCE: CA 125/0772P AND METHODS OF USE THEREOF
CURRENT APPLICATION NUMBER: US/10/687,035
CURRENT FILING DATE: 2003-10-15
PRIOR APPLICATION NUMBER: 60/485,986
PRIOR FILING DATE: 2003-07-10
PRIOR APPLICATION NUMBER: 60/418,828
PRIOR FILING DATE: 2003-10-12
NUMBER OF SEQ ID NOS: 71
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 368.1 heavy chain polypeptide variable region (368.1H)
US-10-687-035-30

Query Match 86.9%; Score 640.5; DB 5; Length 137;
Best Local Similarity 87.6%; Pred. No. 9.1e-50;
Matches 120; Conservative 8; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
DB 61 GKSLEWIGYISCTNGATSYNOKFKKATFTVDTSSSTAYMQLNSLTSEDSAVYYCAR 119
61 GKSLEWIGYISCTNGATSYNOKFKKATFTVDTSSSTAYMQLNSLTSEDSAVYYCAR 120
QY 120 NMVFDYWGQGTLLTVSS 136
121 YSMDFWGGGTSTVYSS 137
DB

RESULT 3
US-10-462-062-153
Sequence 153, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 153
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: Sequence for H chain V region of anti-Tf mouse monoclonal
OTHER INFORMATION: antibody ATR-2
US-10-462-062-153

Query Match 81.6%; Score 601.5; DB 4; Length 137;
Best Local Similarity 83.2%; Pred. No. 2.9e-46;
Matches 114; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
DB 1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
61 GKSLEWIGYISCTNGATSYNOKFKKATFTVDTSSSTAYMQLNSLTSEDSAVYYCARGA- 119

|||||
DB 61 GKSLEWIGYIDPNYNGTITYNOKFKKATITVDKSSSTAFMHLNLSLTSEDSAVYYCARGE 120
QY 120 NMVFDYWGQGTLLTVSS 136
121 GYFDYWGQGTLLTVSS 137
DB

RESULT 4
US-10-462-062-154
Sequence 154, Application US/10462062
Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 154
LENGTH: 137
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Full-length amino acid
OTHER INFORMATION: Sequence for H chain V region of anti-Tf mouse monoclonal
US-10-462-062-154

Query Match 81.6%; Score 601.5; DB 4; Length 137;
Best Local Similarity 83.2%; Pred. No. 2.9e-46;
Matches 114; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
1 MGVWIFLLSTAGVHSEVQLQSGPELVKIGASVKISCKASGYSFTGYMHWKQSH 60
DB 61 GKSLEWIGYISCTNGATSYNOKFKKATFTVDTSSSTAYMQLNSLTSEDSAVYYCARGA- 119
61 GKSLEWIGYIDPNYNGTITYNOKFKKATITVDKSSSTAFMHLNLSLTSEDSAVYYCARGE 120
QY 120 NMVFDYWGQGTLLTVSS 136
121 GYFDYWGQGTLLTVSS 137
DB

RESULT 5
US-10-389-155-60
Sequence 60, Application US/10389155
Publication No. US20030229208A1
GENERAL INFORMATION:
APPLICANT: Queen, Cary L.
Co. Man Sung
Schneider, William P.
Landoft, Nicholas F.
Coeligh, Kathleen L.
Selick, Harold E.
TITLE OF INVENTION: Improved Humanized Immunoglobulins
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:05:40 ; Search time 35.4113 Seconds
(without alignments)
317.523 Million cell updates/sec

Title: US-10-768-193-7
Perfect score: 737
Sequence: 1 MGWMIFFLLISGTRAGVHSE.....RGAMWVFDYMGQTTLVSS 136

Scoring table:
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Gapop 10.0 , Gapext 0.5

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/1aa/backfill1est.pep:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	601.5	81.6	137	2	US-09-647-468-153 Sequence 153, App
2	601.5	81.6	137	2	US-09-647-468-154 Sequence 154, App
3	593.5	80.5	135	1	US-07-634-278-69 Sequence 69, App
4	593.5	80.5	135	1	US-08-477-728-69 Sequence 69, App
5	593.5	80.5	135	1	US-08-474-040-69 Sequence 69, App
6	593.5	80.5	135	1	US-08-487-200-69 Sequence 69, App
7	593.5	80.5	135	1	US-08-137-117D-27 Sequence 27, App
8	593.5	80.5	135	1	US-08-436-717-27 Sequence 27, App
9	593.5	80.5	135	2	US-08-484-537-69 Sequence 69, App
10	564	76.5	138	1	US-07-634-278-85 Sequence 85, App
11	564	76.5	138	1	US-08-477-728-85 Sequence 85, App
12	564	76.5	138	1	US-08-474-040-85 Sequence 85, App
13	564	76.5	138	1	US-08-487-200-85 Sequence 85, App
14	564	76.5	138	2	US-08-484-537-85 Sequence 85, App
15	557	75.6	132	2	US-08-434-000A-14 Sequence 14, App
16	557	75.6	132	2	US-09-312-157-14 Sequence 14, App
17	557	75.6	132	2	US-09-717-888-14 Sequence 14, App
18	555.5	75.4	137	2	US-08-379-057-18 Sequence 18, App
19	554.5	75.2	137	2	US-09-647-468-158 Sequence 158, App
20	554	75.2	142	1	US-08-678-194-8 Sequence 8, App
21	554	75.2	142	2	US-08-890-011-8 Sequence 8, App
22	554	75.2	142	2	US-09-262-724-8 Sequence 8, App
23	551.5	74.8	139	1	US-08-116-778E-1 Sequence 1, App
24	551.5	74.8	139	1	US-08-438-562-1 Sequence 1, App
25	551.5	74.8	139	1	US-08-483-528B-91 Sequence 91, App
26	550.5	74.7	137	1	US-08-116-778E-3 Sequence 3, App
27	550.5	74.7	137	1	US-08-438-562-3 Sequence 3, App

28	550.5	74.7	137	1	US-08-483-528B-93 Sequence 93, App
29	549.5	74.6	124	2	US-09-257-069-2 Sequence 2, App
30	549.5	74.6	124	2	US-10-007-790-2 Sequence 2, App
31	545.5	74.0	137	2	US-09-647-468-157 Sequence 157, App
32	544	73.8	136	2	US-08-525-539A-47 Sequence 47, App
33	544	73.8	140	4	PCT-US93-11612-4 Sequence 4, App
34	542	73.5	140	4	US-08-579-378A-4 Sequence 4, App
35	541.5	73.5	233	2	US-08-444-644-33 Sequence 33, App
36	541.5	73.5	233	2	US-08-232-246A-19 Sequence 19, App
37	541.5	73.5	235	2	US-08-444-644-19 Sequence 19, App
38	541.5	73.5	235	2	US-08-444-644-28 Sequence 28, App
39	541.5	73.5	235	2	US-08-444-644-42 Sequence 42, App
40	541.5	73.5	235	2	US-08-232-246A-19 Sequence 19, App
41	541.5	73.5	235	2	US-08-232-246A-28 Sequence 28, App
42	541.5	73.5	235	2	US-08-232-246A-42 Sequence 42, App
43	534.5	72.5	137	2	US-08-444-644-17 Sequence 17, App
44	534.5	72.5	137	2	US-08-232-246A-17 Sequence 17, App
45	526	71.4	140	2	US-08-836-561-27 Sequence 27, App

ALIGNMENTS

```
RESULT 1
US-09-647-468-153
Sequence 153, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 2000-09-29
PCT FILING DATE: 1999-04-02
PCT APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 153
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-2
US-09-647-468-153
Query Match
Best Local Similarity 81.6%; Score 601.5; DB 2; Length 137;
Matches 114; Conservative 5; Mismatches 17; Indels 1; Gaps 1;
QY 1 MGWMIFFLLISGTRAGVHSEVQLOSGPELYKTGASVYISCKASGYSTGYTHMVKQSH 60
DB 1 KSLSEWIGYIPYNGGTTLVSS 136
QY 61 KSLSEWIGYIPYNGGTTLVSS 136
DB 61 KSLSEWIGYIPYNGGTTLVSS 136
QY 120 MWVPMGQTTLVSS 136
DB 120 GYVPMGQTTLVSS 137
RESULT 2
US-09-647-468-154
Sequence 154, Application US/09647468
Patent No. 6677436
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GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: YABUTA, NAOHITO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
LENGTH: 137
TYPE: PRT
ORGANISM: Mus sp.
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence coding for H chain V region of ant-TF
OTHER INFORMATION: mouse monoclonal antibody ATR-3
US-09-647-468-154

Query Match 81.6%; Score 601.5; DB 2; Length 137;
Best Local Similarity 83.2%; Pred. No. 5.5e-48;
Matches 114; Conservative 5; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGMIWIFLLISGTAHVSEVLOOOSGPELVKTGASVKSCKASGYSTGYMMHWKQSH 60
1 MEMSWIFLLISGTAHVSEVLOOOSGPELVKPGASVKSCKASGYSTGYMMHWKQSH 60
DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMFPNSLTSEDSAVYYCARGA- 119
61 GKSLEWIGYIDPYNGGTYINQKFKGKATITVTKSSSTAFMHLNSLTSEDSAVYYCARGE 120
QY 120 NWFDYWGQGTTLTVSS 136
121 GYFDYWGQGTTLTVSS 137
DB 121 GYFDYWGQGTTLTVSS 137

RESULT 3
US-07-634-278-69
Sequence 69, Application US/07634278
Patent No. 5530101
GENERAL INFORMATION:
APPLICANT: QUEEN, Gary L.
APPLICANT: CO, Man Sung
APPLICANT: SCHNEIDER, William P.
APPLICANT: LANDOLFI, Nicholas F.
APPLICANT: COELINGH, Kathleen L.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: 379 Lytton Avenue
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/634,278
FILING DATE: 19-DEC-1990
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274

FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252
FILING DATE: 13-FEB-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/290,975
FILING DATE: 28-DEC-1988
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-002600
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 326-2400
TELEFAX: (415) 326-2422
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-634-278-69

Query Match 80.5%; Score 593.5; DB 1; Length 135;
Best Local Similarity 83.8%; Pred. No. 2.9e-47;
Matches 114; Conservative 3; Mismatches 18; Indels 1; Gaps 1;

QY 1 MGMIWIFLLISGTAHVSEVLOOOSGPELVKTGASVKSCKASGYSTGYMMHWKQSH 60
1 MEMSWIFLLISGTAHVSEVLOOOSGPELVKPGASVKSCKASGYSTGYMMHWKQSH 60
DB 61 GKSLEWIGYISCVNGATSYNOKFKGKATFTVDTSSSTAYMFPNSLTSEDSAVYYCARGAN 120
61 GKSLEWIGYIDPYNGGTYINQKFKGKATITVTKSSSTAFMHLNSLTSEDSAVYYCARGP 120
QY 121 NWFDYWGQGTTLTVSS 136
121 NWFDYWGQGTTLTVSS 135
DB 121 NWFDYWGQGTTLTVSS 135

RESULT 4
US-08-477-728-69
Sequence 69, Application US/08477728
Patent No. 5585089
GENERAL INFORMATION:
APPLICANT: QUEEN, Gary L.
APPLICANT: SCHNEIDER, William P.
APPLICANT: SELICK, Harold E.
TITLE OF INVENTION: IMPROVED HUMANIZED IMMUNOGLOBULINS
NUMBER OF SEQUENCES: 113
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: Palo Alto
STATE: California
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,728
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/634,278
FILING DATE: 19-DEC-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/590,274
FILING DATE: 28-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/310,252

PI Yanagisawa K, Shibata M;
 XX WPI; 2003-268182/26.
 DR N-PSDB; ABX93689.
 XX
 XX Antibodies recognizing GM1 ganglioside-bound amyloid beta-protein and
 PT encoded DNA, useful in diagnosing, preventing or treating Alzheimer's
 XX disease by inhibiting early-stage beta-amyloid fibril formation.
 XX
 PS Claim 5; Fig 2; 60pp; Japanese.
 CC The invention relates to four antibodies recognising GM1 ganglioside-
 CC bound amyloid beta protein and having inhibitory activity on the
 CC formation of amyloid fibril. The antibodies are useful in diagnosing,
 CC preventing or treating Alzheimer's disease by inhibiting early-stage beta
 CC -amyloid fibril formation. The antibody does not recognise soluble
 CC amyloid beta-protein, and thus drugs produced from the antibodies are
 CC efficacious in treating Alzheimer's disease. The present sequence
 CC represents the amino acid sequence of mouse GM1 ganglioside-bound amyloid
 CC beta antibody light chain variable region
 XX
 SQ Sequence 129 AA;
 Query Match 100.0%; Score 668; DB 6; Length 129;
 Best Local Similarity 100.0%; Pred. No. 3.4e-51;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MAMTSLILSLALCSGASQAVVTQESALTSPGTVILTCRSSGATTSNYANWQEK 60
 DB 1 MAMTSLILSLALCSGASQAVVTQESALTSPGTVILTCRSSGATTSNYANWQEK 60
 QY 61 PDHLFTGLIGTSNRAPGVPRFSGSLIGDKAALITGAQTEDDAMFYCALWYTHYVFG 120
 DB 61 PDHLFTGLIGTSNRAPGVPRFSGSLIGDKAALITGAQTEDDAMFYCALWYTHYVFG 120
 QY 121 GGTXYTVLG 129
 DB 121 GGTXYTVLG 129
 RESULT 2
 AAR09422
 ID AAR09422 standard; protein; 131 AA.
 XX
 AC AAR09422;
 XX
 DT 25-MAR-2003 (revised)
 DT 04-MAR-1993 (first entry)
 XX
 DE Br-3 Light Chain V Region (mouse).
 XX
 KW Monoclonal antibody; chimera; light; heavy; chain; constant; variable;
 KW antigen; diagnosis; cancer; tumour.
 XX
 OS Mus musculus.
 XX
 PN WO9002569-A.
 XX
 PD 22-MAR-1990.
 XX
 PF 08-SEP-1988; 88US-00241744.
 XX
 PR 08-SEP-1988; 88US-00241744.
 PR 13-SEP-1988; 88US-00243739.
 PR 04-OCT-1988; 88US-00253002.
 PR 19-JUN-1989; 89US-00367641.
 PR 21-JUL-1989; 89US-00382768.
 XX
 PA (ITGE-) INT GENETIC ENG INC.
 PA (INGE-) INGENE INT GENETIC.
 XX
 PI Better MD, Horwitz AH, Robinson RR, Lei S, Chang CP;
 XX

DR WPI; 1990-115825/15.
 DR N-PSDB; AAM06604.
 XX
 XX Chimeric mouse-human antibodies - prep'd. using genes coding for constant
 PT human region murine variable region, esp. to 3 tumour antigen.
 XX
 PS Claim 13; Page 123 + Fig 14; 173pp; English.
 CC The sequence is used in the prodn. of a chimeric antibody mol. comprising
 CC two light chains and two heavy chains, each having a constant region
 CC (human) and a variable region (murine) having specificity to an antigen
 CC bound by murine monoclonal antibody (MAb) Br-3. The chimeric antibodies
 CC can be used for any purpose for which the original murine MAbs can be
 CC used, with the advantage that they are more compatible with the human
 CC body. They are esp. used for the diagnosis and treatment of cancer.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 131 AA;
 Query Match 90.0%; Score 601; DB 2; Length 131;
 Best Local Similarity 89.9%; Pred. No. 2.9e-45;
 Matches 116; Conservative 5; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MAMTSLILSLALCSGASQAVVTQESALTSPGTVILTCRSSGATTSNYANWQEK 60
 DB 1 MAMTSLILSLALCSGASQAVVTQESALTSPGTVILTCRSSGATTSNYANWQEK 60
 QY 61 PDHLFTGLIGTSNRAPGVPRFSGSLIGDKAALITGAQTEDDAMFYCALWYTHYVFG 120
 DB 61 PDHLFTGLIGTSNRAPGVPRFSGSLIGDKAALITGAQTEDDAMFYCALWYTHYVFG 120
 QY 121 GGTXYTVLG 129
 DB 121 GGTXYTVLG 129
 RESULT 3
 AAM06211
 ID AAM06211 standard; protein; 131 AA.
 XX
 AC AAM06211;
 XX
 DT 25-MAR-2003 (revised)
 DT 12-FEB-1997 (first entry)
 XX
 DE MAb Br-3 light chain variable region.
 XX
 KW Chimeric antibody; monoclonal antibody; Br-3; antibody engineering;
 KW tumour; antigen; breast carcinoma; lung carcinoma; colon carcinoma;
 KW ovary carcinoma; cancer; diagnosis; therapy; light chain.
 XX
 OS Mus sp.
 XX
 PN US5576184-A.
 XX
 PD 19-NOV-1996.
 XX
 PF 27-DEC-1994; 94US-00364001.
 XX
 PR 06-SEP-1988; 88US-00240624.
 PR 08-SEP-1988; 88US-00241744.
 PR 13-SEP-1988; 88US-00243739.
 PR 04-OCT-1988; 88US-00253002.
 PR 19-JUN-1989; 89US-00367641.
 PR 21-JUL-1989; 89US-00382768.
 PR 06-MAY-1991; 91US-00659401.
 XX
 PA (XOMA) XOMA CORP.
 XX
 PI Chang CP, Lei S, Better MD, Robinson RR, Horwitz AH;
 XX
 DR WPI; 1997-011249/01.
 DR N-PSDB; AAT43436.

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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:00:46 ; Search time 23.8528 Seconds
(without alignments)
520.356 Million cell updates/sec

Title: US-10-768-193-8

Perfect score: 668
Sequence: 1 MAWSTSLSLALCSGASQ.....ALWSTHYFGGTRVTLG 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	649	97.2	129	1 L2MS35	Ig lambda-2 chain
2	603	90.3	117	1 L2MSWE	Ig lambda-2 chain
3	599	89.7	128	1 S52450	Ig lambda chain V
4	597	89.4	129	1 LMS4E	Ig lambda-1 chain
5	545	81.6	116	1 LMSV	Ig lambda-1 chain
6	529	79.2	287	4 PC4402	pe1B leader/Ig hea
7	525	78.6	100	2 PH1087	Ig lambda chain V
8	518	77.5	113	2 S06819	Ig lambda chain V
9	514	76.9	214	2 PC4156	Ig lambda chain V
10	511.5	76.6	112	2 S06818	Ig lambda chain V
11	506.5	75.8	114	2 S06820	Ig lambda chain V
12	506	75.7	106	2 S20654	Ig lambda chain V
13	503	75.3	99	2 S14583	Ig lambda chain V
14	497.5	74.5	114	2 S06822	Ig lambda chain V
15	492	73.7	113	2 BS4256	Ig lambda chain V
16	492	73.7	113	2 S06821	Ig lambda chain V
17	485	72.6	92	2 A27633	Ig lambda chain V
18	482	72.2	116	2 C27390	Ig lambda chain pr
19	477	71.4	99	2 S14582	Ig lambda chain V
20	475	71.1	97	2 PH1090	Ig lambda chain V
21	475	71.1	100	2 PH1088	Ig lambda chain V
22	470	70.4	99	2 S14584	Ig lambda chain V
23	469.5	70.3	99	2 PH1089	Ig lambda chain V
24	454	68.0	99	2 S14586	Ig lambda chain V
25	444	66.0	99	2 S14585	Ig lambda chain V
26	351.5	52.6	136	2 S42610	ARKVlambda protein
27	348	52.1	117	2 S04526	Ig lambda chain pr
28	339.5	50.8	117	1 LVH02	Ig lambda chain pr
29	336.5	50.4	235	2 S25749	Ig lambda chain -

30	302.5	45.3	120	2 S30528	Ig lambda chain V
31	289.5	43.3	127	2 S70444	Ig lambda chain pr
32	289	43.3	128	2 S36062	Ig lambda chain V
33	289	43.3	112	2 S26655	Ig lambda chain V
34	287.5	43.0	110	2 S57465	Ig lambda chain V
35	283.5	42.4	233	2 S25741	Ig lambda chain -
36	282.5	42.3	231	2 S25738	Ig lambda chain -
37	273.5	40.9	151	2 S25739	Ig lambda chain -
38	267.5	40.0	231	2 S25751	Ig lambda chain -
39	265.5	39.9	233	2 S25748	Ig lambda chain -
40	265.5	39.7	233	2 S25747	Ig lambda chain -
41	264.5	39.6	128	2 S24319	Ig lambda chain pr
42	264	39.5	98	2 S36063	Ig lambda chain -
43	262	39.2	235	2 S25754	Ig lambda chain -
44	260.5	39.0	132	2 S09713	Ig lambda chain V
45	260.5	39.0	233	2 S25744	Ig lambda chain -

ALIGNMENTS

RESULT 1
L2MS35
Ig lambda-2 chain precursor V region (MOPC 315) - mouse
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1980 #sequence revision 01-Dec-1995 #text change 09-Jul-2004
C.Accession: A93431; B93282; E91462; A90372; A90410; S09391; A01997
R.Wu, G.E.; Govindji, N.; Hozumi, N.; Murialdo, H.
Nucleic Acids Res. 10, 3831-3843, 1982
A.Title: Nucleotide sequence of a chromosomal rearranged lambda-2 immunoglobulin gene of A.Reference number: A93431; MUID:82274221; PMID:6287422
A.Accession: A93431
A.Molecule type: mRNA
A.Residues: 1-129 <WDG>
A.Cross-references: UNIPROT:P01729; UNIPARC:UP100000270BD
R.Bohwell, A.L.M.; Paskind, M.; Rech, M.; Imantsht-Kart, T.; Rajewsky, K.; Baltimore, D. Nature 298, 380-382, 1982
A.Title: Somatic variants of murine immunoglobulin lambda light chains.
A.Reference number: A93282; MUID:82220143; PMID:6283385
A.Accession: B93282
A.Molecule type: DNA
A.Residues: 1-129 <BOT>
A.Cross-references: UNIPARC:UP100000270BD
A.Note: The sequence was determined from the differentiated gene
R.Schlechter, I.; Wolf, O.; Zemell, R.; Bursstein, Y. Fed. Proc. 38, 1839-1845, 1979
A.Title: Structure and function of immunoglobulin genes and precursors.
A.Reference number: A91462; MUID:79148758; PMID:428562
A.Accession: B91462
A.Molecule type: protein
A.Residues: 1-22 <SCH>
A.Cross-references: UNIPARC:UP10000173724
R.Dugan, E.S.; Bradshaw, R.A.; Simms, E.S.; Eisen, H.N. Biochemistry 12, 5400-5416, 1973
A.Title: Amino acid sequence of the light chain of a mouse myeloma protein (MOPC-315).
A.Reference number: A90372; MUID:74048693; PMID:4760498
A.Accession: A90372
A.Molecule type: protein
A.Residues: 20-24, 'E', '26-73', 'D', '75-129 <DUG>
A.Cross-references: UNIPARC:UP10000173725
R.Gavish, M.; Zakut, R.; Wilchek, M.; Givol, D. Biochemistry 17, 1345-1351, 1978
A.Title: Preparation of a semisynthetic antibody.
A.Reference number: A90410; MUID:78187254; PMID:418802
A.Accession: A90410
A.Molecule type: protein
A.Residues: 1-129 <GAV>
A.Cross-references: UNIPARC:UP100000270BD
R.Boogen, B.; Lambdis, J.D. EMBO J. 8, 1947-1952, 1989
A.Title: Minimum length of an idiotype peptide and a model for its binding to a major h A.Reference number: S09391; MUID:90065397; PMID:2792076
A.Accession: S09391

A/Molecule type: protein
 A/Residues: 110-126 <BOG>
 A/Cross-references: UNIPARC:UPI0000173726
 C/Comment: This chain is from a myeloma protein with anti-DNP activity.
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; pyroglutamic acid
 F.1-19/Domain: signal sequence #status experimental <SIG>
 F.20-129/Domain: Ig lambda-2 chain precursor V region #status experimental <MAT>
 F.34-111/Domain: immunoglobulin homology <IMM>
 F.110-126/Region: idio type to histocompatibility complex class II #status experimental
 F.20/Modified site: pyroglutamic acid (Gln) (in mature form) #status experimental
 F.41-109/Disulfide bonds: #status predicted

Query Match 97.2%; Score 649; DB 1; Length 129;
 Best Local Similarity 96.1%; Pred. No. 1.2e-48;
 Matches 124; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 DB 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 QY 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHYVFG 120
 DB 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHYVFG 120
 QY 121 GGTAKTVLIG 129
 DB 121 GGTAKTVLIG 129

RESULT 2
 L2MSWE
 Ig lambda-2 chain precursor V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 30-Nov-1980 #sequence_revision 30-Nov-1980 #text_change 09-Jul-2004
 C/Accession: A01996
 R/Tonegawa, S.; Maxam, A.M.; Tizard, R.; Bernard, O.; Gilbert, W.
 Proc. Natl. Acad. Sci. U.S.A. 75, 1485-1489, 1978
 A/Title: Sequence of a mouse germ-line gene for a variable region of an immunoglobulin 1
 A/Reference number: A01996; MUID:78179064; PMID:418414
 A/Accession: A01996
 A/Molecule type: DNA
 A/Residues: 1-117 <TON>
 A/Cross-references: UNIPROT:P01728; UNIPARC:UPI0000021FB0; GB:V00815; NID:952278; PIDN:C
 A/Note: the sequence was determined from the germ-line gene
 C/Genetics:
 A/Introns: 16/1
 C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin; pyroglutamic acid
 F.1-19/Domain: signal sequence #status predicted <SIG>
 F.20-117/Domain: Ig lambda-2 chain V region #status predicted <MAT>
 F.34-111/Domain: immunoglobulin homology <IMM>
 F.20/Modified site: pyroglutamic acid (Gln) (in mature form) #status predicted
 F.41-109/Disulfide bonds: #status predicted

Query Match 90.3%; Score 603; DB 1; Length 117;
 Best Local Similarity 99.1%; Pred. No. 9e-45;
 Matches 116; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 DB 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 QY 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHY 117
 DB 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHY 117

RESULT 3

S52450
 Ig lambda chain V region - mouse
 C/Species: Mus musculus (house mouse)
 C/Date: 08-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C/Accession: S52450
 R/Berdoz, U.; Kraehenbuhl, J.P.
 Submitted to the EMBL Data Library, November 1994
 A/Description: Specific amplification by the polymerase chain reaction of rearranged gene
 A/Reference number: S52445
 A/Accession: S52450
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-128 <BER>
 A/Cross-references: UNIPARC:UPI0000114EBF; EMBL:X82687; NID:9673448; PIDN:CAA58008.1; PII
 C/Genetics:
 A/Introns: 16/1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: heterotetramer; immunoglobulin
 F.34-111/Domain: immunoglobulin homology <IMM>

Query Match 89.7%; Score 599; DB 2; Length 128;
 Best Local Similarity 90.6%; Pred. No. 2.2e-44;
 Matches 116; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 DB 1 MAMTSLIISLALCGASSQAVVTQESALTTPGCTVILTCRSSGTGAVTTSNYANWQEK 60
 QY 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHYVFG 120
 DB 61 PDHLFTGLIGTGNRPAQVPRFSGSLIGDKAALTITGAQTEDDAMFYCALWYSTHYVFG 120
 QY 121 GGTAKTVL 128
 DB 121 GGTAKTVL 128

RESULT 4
 L2MS4E
 Ig lambda-1 chain precursor V regions (MOPC 104E, RPC20, J558, S104, S178, H2020, S43) -
 C/Species: Mus musculus (house mouse)
 C/Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 09-Jul-2004
 R/Burstein, Y.; Schechter, I.
 Proc. Natl. Acad. Sci. U.S.A. 74, 716-720, 1977
 A/Title: Amino acid sequence of the NH-2-terminal extra piece segments of the precursors
 A/Reference number: A93815; MUID:77148916; PMID:403522
 A/Contents: MOPC 104E
 A/Accession: B93815
 A/Molecule type: protein
 A/Residues: 1-29 <BUR>
 A/Cross-references: UNIPROT:P01724; UNIPARC:UPI0000173721
 A/Note: this precursor was synthesized in a cell-free system directed by messenger RNA in
 d after synthesis
 R/Appella, E.
 Proc. Natl. Acad. Sci. U.S.A. 69, 590-594, 1971
 A/Title: Amino acid sequences of two mouse immunoglobulin lambda chains.
 A/Reference number: A93775; MUID:71107854; PMID:5276767
 A/Contents: MOPC 104E; RPC 20
 A/Accession: B93775
 A/Molecule type: protein
 A/Residues: 1-25, 27-129 <APP>
 A/Cross-references: UNIPARC:UPI0000173722
 A/Accession: C93775
 A/Molecule type: protein
 A/Residues: 20-129 <AP2>
 A/Cross-references: UNIPARC:UPI0000173722
 A/Note: compositions and partial sequences of RPC 20 show no differences from MOPC 104E
 R/Cesari, I.M.; Weigert, M.
 Proc. Natl. Acad. Sci. U.S.A. 70, 2112-2116, 1973
 A/Title: Mouse lambda-chain sequences.
 A/Reference number: A93784; MUID:73229669; PMID:4516208
 A/Contents: J558; S104; S178

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OM protein - protein search, using sw model

Run on: March 21, 2006, 17:50:40 ; Search time 143.604 Seconds
(without alignments)
633.780 Million cell updates/sec

Title: US-10-768-193-8

Perfect score: 668

Sequence: 1 MAMTSJLSLALCSGASQ.....ALMSTHYVFGGKRVTLG 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	649	97.2	129	1	LV2B_MOUSE
2	605	90.6	129	1	LV1E_MOUSE
3	603	90.3	117	1	LV2A_MOUSE
4	598	89.5	129	1	LV1D_MOUSE
5	597	89.4	129	1	LV1B_MOUSE
6	593	88.8	129	2	OBVDE2_MOUSE
7	534.5	80.0	117	1	LV1A_MOUSE
8	510	76.3	110	1	LV1C_MOUSE
9	509.5	76.3	113	2	OBGGS1_MOUSE
10	495.5	74.2	109	2	OGETI3_MOUSE
11	366	54.8	234	2	OSGZ94_HUMAN
12	339.5	50.8	117	1	LVDA_HUMAN
13	291	43.6	98	2	OSNV60_HUMAN
14	287	43.0	98	2	OSNV83_HUMAN
15	276.5	41.4	233	2	OGMW4_HUMAN
16	276	41.3	236	2	OGMX4_HUMAN
17	273.5	40.9	231	2	OGNB8_XENLA
18	270.5	40.5	248	2	OZSYU1_XENLA
19	270	40.4	236	2	OGMW7_HUMAN
20	268.5	40.2	233	2	OBTCB9_HUMAN
21	268.5	40.2	245	2	OGNCS_XENLA
22	268	40.1	233	2	OGPUJ3_HUMAN
23	265.5	39.7	235	2	OGPIK1_HUMAN
24	265	39.7	235	2	OGPEB1_HUMAN
25	265	39.7	236	2	OGPI07_HUMAN
26	264.5	39.6	233	2	OGNSF4_HUMAN
27	264	39.5	99	2	OSNV62_HUMAN
28	264	39.5	236	2	OGIPD0_HUMAN
29	262	39.2	236	2	OGPS63_HUMAN
30	262	39.2	236	2	OGNEJ1_HUMAN
31	260	38.9	236	2	OGMX3_HUMAN

32	259	38.8	131	1	LV6E_HUMAN	P06319	homo sapien
33	259	38.8	232	2	OSFWF9_HUMAN	Q5WF9	homo sapien
34	255	38.2	234	2	Q8N355_HUMAN	Q8N355	homo sapien
35	254.5	38.1	235	2	Q567P1_HUMAN	Q567P1	homo sapien
36	253.5	37.9	233	2	OGGNH3_XENLA	Q6GNH3	homo sapien
37	252.5	37.8	130	1	LV1G_HUMAN	Q6GNH3	homo sapien
38	252.5	37.8	235	2	OGGMW6_HUMAN	Q6GMW6	homo sapien
39	251	37.6	234	2	OGGMW3_HUMAN	Q6GMW3	homo sapien
40	249.5	37.4	235	2	OGIN99_HUMAN	Q6IN99	homo sapien
41	248	37.1	234	2	OGMW8_HUMAN	Q6MW8	homo sapien
42	246.5	36.9	233	2	OGNS96_HUMAN	Q6NS96	homo sapien
43	246.5	36.9	235	2	OGPIJ0_HUMAN	Q6PIJ0	homo sapien
44	240.5	36.0	111	1	LV6C_HUMAN	P06317	homo sapien
45	240.5	36.0	148	2	OGPJ28_HUMAN	Q6PJ28	homo sapien

ALIGNMENTS

```

RESULT 1
LV2B_MOUSE
ID LV2B_MOUSE STANDARD; PRT; 129 AA.
AC P01729;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Ig lambda2 chain V region WOPC 315 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82274221; Pubmed=6287422;
RA Wu G.E., Govindji N., Hozumi N., Murialdo H.;
RT "Nucleotide sequence of a chromosomal rearranged lambda 2
immunoglobulin gene of mouse."
RL Nucleic Acids Res. 10:3831-3843(1982).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=82220143; Pubmed=6283385;
RA Botchwell A.L.M., Pasikind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RL Baltimore D.;
RT "Somatic variants of murine immunoglobulin lambda light chains."
RN [3]
RP PROTEIN SEQUENCE OF 1-22.
RX MEDLINE=79148758; Pubmed=428562;
RA Schechter I., Wolf O., Zemell R., Burstein Y.;
RT "Structure and function of immunoglobulin genes and precursors."
RL Fed. Proc. 38:1839-1845(1979).
RN [4]
RP PROTEIN SEQUENCE OF 20-129.
RX MEDLINE=74048693; Pubmed=4760498;
RA Dugan E.S., Bradshaw R.A., Simms E.S., Eisen H.N.;
RT "Amino acid sequence of the light chain of a mouse myeloma protein
(MOPC-315)."
RL Biochemistry 12:5400-5416(1973).
RN [5]
RP DETERMINATION OF ANTIHATION STATES OF 58; 59; 62; 100; 102 AND 115.
RX MEDLINE=78187254; Pubmed=418802;
RA Gavish M., Zakut R., Wilchek M., Givol D.;
RT "Preparation of a semisynthetic antibody."
RL Biochemistry 17:1345-1351(1978).
-1- MISCELLANEOUS: This chain is from a myeloma protein with anti-DNP
activity.
-1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
-----
This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
DR PIR; A93431; L2M635.
DR HSSP; P01724; 1A6V.
DR SMR; P01729; 20-129.
DR Ensembl; ENSMUSG0000064012; Mus musculus.
DR InterPro; IPR002197; HTH_Fls.
DR InterPro; IPR003596; IG_V.
DR PRINTS; PRO1590; HTHFIS.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Direct protein sequencing; Immunoglobulin domain;
KW Immunoglobulin V region; Pyrolysine carboxylic acid; Signal.
FT SIGNAL 1 19
FT CHAIN 20 129 Ig lambda-2 chain V region MOPC 315.
FT DOMAIN 20 125 Ig-like.
FT MOD_RES 20 20 Pyrolysine carboxylic acid.
FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13418 MW; 0AA6B8125723552C CRC64;

Query Match
Best Local Similarity 97.2%; Score 649; DB 1; Length 129;
Matches 124; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MAMTSLIISLALCGASQAQAVTQESALTTPSGTVILTCRSSGAVTTSNYANWQEK 60
DB 1 MAMTSLIISLALCGASQAQAVTQESALTTPSGTVILTCRSSGAVTTSNYANWQEK 60
OY 61 PDHLFTGLIGSTNRAPGVPRFSGSLIGDKAALTITGAQEDDAMVFCALMYSTHYVFG 120
DB 61 PDHLFTGLIGSTNRAPGVPRFSGSLIGDKAALTITGAQEDDAMVFCALMYSTHYVFG 120
OY 121 GGTATVVLG 129
DB 121 GGTATVVLG 129

RESULT 2
LV1E MOUSE
ID LV1E MOUSE STANDARD; PRT; 129 AA.
AC P01727;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DR Ig lambda-1 chain V region S43 precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC Muridae; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC MEDLINE=82220143; PubMed=6283385;
CC Botwell A.L.M., Paekind M., Rech M., Imanishi-Kari T., Rajewsky K.,
CC Baltimore D.;
CC "Somatic variants of murine immunoglobulin lambda light chains.";
CC Nature 298:380-382(1982).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC HSSP; P01724; 1A6V.
CC SMR; P01727; 20-129.
CC Ensembl; ENSMUSG0000064012; Mus musculus.
CC InterPro; IPR007110; IG_LIKE.
CC InterPro; IPR003596; IG_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig lambda-2 chain V region.
FT DOMAIN 20 >117 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12222 MW; 43FDF197419B42A6 CRC64;

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KW Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
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FT NON_TER 129 129
SQ SEQUENCE 129 AA; 13529 MW; 84E54E7DD5791345 CRC64;

Query Match
Best Local Similarity 90.6%; Score 605; DB 1; Length 129;
Matches 117; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

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DB 1 MAMTSLIISLALCGASQAQAVTQESALTTPSGTVILTCRSSGAVTTSNYANWQEK 60
OY 61 PDHLFTGLIGSTNRAPGVPRFSGSLIGDKAALTITGAQEDDAMVFCALMYSTHYVFG 120
DB 61 PDHLFTGLIGSTNRAPGVPRFSGSLIGDKAALTITGAQEDDAMVFCALMYSTHYVFG 120
OY 121 GGTATVVLG 129
DB 121 GGTATVVLG 129

RESULT 3
LV2A MOUSE
ID LV2A MOUSE STANDARD; PRT; 117 AA.
AC P01728;
DR 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DR 10-MAY-2005 (Rel. 47, Last annotation update)
DR Ig lambda-2 chain V region precursor.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
CC Muridae; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
CC [1]
CC NUCLEOTIDE SEQUENCE.
CC MEDLINE=78179064; PubMed=418414;
CC Tonegawa S., Maxam A.M., Tizard R., Bernard O., Gilbert W.;
CC "Sequence of a mouse germ-line gene for a variable region of an
CC immunoglobulin light chain.";
CC Proc. Natl. Acad. Sci. U.S.A. 75:1485-1489(1978).
CC -1- SIMILARITY: Contains 1 Ig-like (immunoglobulin-like) domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; J00599; AAA39167.1; -; Genomic DNA.
CC EMBL; V00815; CAA24196.2; -; Genomic DNA.
CC EMBL; X58412; CAA41313.1; -; Genomic DNA.
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CC EMBL; X58424; CAA41324.1; -; Genomic DNA.
CC PIR; A01996; L2M635.
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CC SMR; P01728; 20-117.
CC Ensembl; ENSMUSG0000064012; Mus musculus.
CC InterPro; IPR007110; IG_LIKE.
CC InterPro; IPR003596; IG_V.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
CC Immunoglobulin domain; Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 Ig lambda-2 chain V region.
FT DOMAIN 20 >117 Ig-like.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12222 MW; 43FDF197419B42A6 CRC64;

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:05:40 ; Search time 33.5887 Seconds
(without alignments)
317.523 Million cell updates/sec

Title: US-10-768-193-8

Perfect score: 668
Sequence: 1 MAMTSLILSLALCGASSQ.....ALWYTHYVGGGTXTVVG 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Issued Patents AA:*
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5: /cgn2_6/prodata/1/iaa/FR COMB.pep:*
6: /cgn2_6/prodata/1/iaa/Backfill61.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	597	89.4	128	2	US-08-348-548-2
2	597	89.4	128	4	PCT-US95-15716-2
3	552	82.6	115	6	5215889-3
4	545	81.6	269	1	US-08-428-257A-72
5	545	81.6	269	1	US-08-491-988-3
6	545	81.6	402	1	US-08-491-988-9
7	545	81.6	415	1	US-08-491-988-7
8	545	81.6	435	1	US-08-491-988-5
9	535	80.1	112	2	US-09-157-370-6
10	512	76.6	109	2	US-09-232-290-14
11	507	75.9	110	1	US-08-122-546-14
12	507	75.9	110	1	US-08-764-938-14
13	507	75.9	110	2	US-09-131-052-14
14	507	75.9	110	2	US-09-131-053A-14
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17	495.5	74.2	109	2	US-10-726-555-7
18	495	74.1	106	1	US-08-440-354-2
19	495	74.1	106	1	US-08-463-087-2
20	490	73.4	109	1	US-08-672-345C-1
21	490	73.4	109	2	US-09-214-095D-1
22	490	73.4	109	2	US-09-940-727B-1
23	486	72.8	109	1	US-08-672-345C-2
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25	486	72.8	109	2	US-09-940-727B-2
26	477	71.4	109	1	US-08-672-345C-3
27	477	71.4	109	2	US-09-214-095D-3

28	477	71.4	109	2	US-09-214-095D-121	Sequence 121, App
29	477	71.4	109	2	US-09-940-727B-3	Sequence 3, Appl
30	477	71.4	109	2	US-09-940-727B-121	Sequence 121, App
31	475	71.1	109	1	US-08-672-345C-93	Sequence 93, Appl
32	462	69.2	109	1	US-08-672-345C-4	Sequence 4, Appl
33	446	66.8	99	1	US-08-672-345C-91	Sequence 91, Appl
34	446	66.8	99	2	US-09-214-095D-92	Sequence 92, Appl
35	446	66.8	99	2	US-09-940-727B-92	Sequence 92, Appl
36	442	66.2	99	2	US-09-214-095D-88	Sequence 88, Appl
37	442	66.2	99	2	US-09-940-727B-88	Sequence 88, Appl
38	442	66.2	200	6	5189147-10	Patent No. 5189147
39	423.5	63.4	99	1	US-08-672-345C-92	Sequence 92, Appl
40	414	62.0	100	2	US-09-214-095D-96	Sequence 96, Appl
41	414	62.0	100	2	US-09-940-727B-96	Sequence 96, Appl
42	412	61.7	98	1	US-08-672-345C-94	Sequence 94, Appl
43	402	60.2	98	2	US-09-214-095D-4	Sequence 4, Appl
44	402	60.2	98	2	US-09-940-727B-4	Sequence 4, Appl
45	368.5	55.2	240	2	US-09-049-672A-11	Sequence 11, Appl

ALIGNMENTS

RESULT 1
US-08-348-548-2
Sequence 2, Application US/08348548
Patent No. 6258529
GENERAL INFORMATION:
APPLICANT: Berdoz, Jose
TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
NUMBER OF SEQUENCES: 108
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street, Suite 3100
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/348,548
FILING DATE: 01-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 06132/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-5070
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 128 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-348-548-2

Query Match 89.4%; Score 597; DB 2; Length 128;
Best Local Similarity 90.6%; Pred. No. 4.4e-50;
Matches 116; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

QY 1 MAMTSLILSLALCGASSQAVVTQESALTTSPGTVILTCRSSGTGAVTTSNYANWQEK 60
DB 1 MAMTSLILSLALCGASSQAVVTQESALTTSPGTVILTCRSSGTGAVTTSNYANWQEK 60

D _b	61	PDLFLFGLLGGISTNRAPGVPAVFSSLLGDKKAALITGAQTEEDAMAFCAALMTSTHYVFG	120
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D _b	61	PDLFLFGLLGGISTNRAPGVPAVFSSLLGDKKAALITGAQTEEDATYFCALWTSNHNVFG	120
Q _y	121	GGRKRVTL	128
D _b	121	GGRKRLTVL	128

RESULT 2
PCT-US95-15716-2
; sequence 2, Application PC/TUS9515716

APPLICANT: Berdoz, Jose
 APPLICANT: Kraehenbuhl, Jean Pierre
 TITLE OF INVENTION: PCR AMPLIFICATION OF REARRANGED GENOMIC
 TITLE OF INVENTION: VARIABLE REGIONS OF IMMUNOGLOBULIN GENES
 NUMBER OF SEQUENCES: 108
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street, Suite 3100
 CITY: Boston
 STATE: MA
 COUNTRY: USA
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30B
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US95/15716
 FILING DATE:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/348,548
 FILING DATE: 01-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 06132/009001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-5070
 TELEEX: 200154
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 128 amino acids
 TYPE: amino acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: protein

Query Match	89.4%	Score	597	DB	4	Length	128
Best Local Similarity	90.6%	Pred	NO	4.4e-50			
Matches	16	Conservative	4	Mismatches	8	Indels	0
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Qy	61	PDHLPLFGILGGISNRA PGVVRPFGSLIGDPAKALITTSAGTEDDAMFCAIMWSTHYVG	120
Db	61	PDHLPLFGILGGITNNRA PGVVRPFGSLIGDKRALITTSAGTEDEATFCALMISNHWVFG	120
Qy	121	GGTKVTVL	128
Db	121	GGTKVTVL	128

RESULT 3
5215889-3
;Patent No. 5215889

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; APPLICANT: SCHULTZ, PETER
; TITLE OF INVENTION: CATALYTIC AND REACTIVE POLYPEPTIDES
; AND METHODS FOR THEIR PREPARATION AND USE
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/404,920
; FILING DATE: 08-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 273,455
; FILING DATE: 18-NOV-1988
; SEQ ID NO: 3
; LENGTH: 115
5215889-3

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Query Match	82.6%;	Score 552;	DB 6;	Length 115;
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Matches 104;	Conservative 3;	Mismatches 2;	Indels 0;	Gaps 0;

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QY      81 VRFGSLIGDKAALTITGAQTEDDAMYFCALMYSTHYVFGGSIKVTVLG  129
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Sequence 72, Application US/08428257A

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Best Local Similarity	90.4%	Pred. No. 1.1e-44;		
Matches 103; Conservative	5;	Mismatches	6;	Indels 0; Gaps 0;

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Db      154 GGGSQAVVTQESALTTPSGTIVILTCRSSIGAVTTSNYANVVOEKDHLFTGLIGTSNR 213

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Db

QY		76
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214	AGGVPARFSGSLIGDKALTTGAQTEDBAIYFCALMYSNNHVFGGGTCLTVLG	267

RESULT 3
5215889-3
;Patent No. 5215889

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 21, 2006, 18:06:30 ; Search time 116.343 Seconds

(without alignments)
463.284 Million cell updates/sec

Title: US-10-768-193-8

Perfect score: 668
Sequence: 1 MAWTSILSLALCSGASSQ.....ALMSTHYVFGGKTVTLG 129

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	535	80.1	112	5	US-10-816-938-8
3	531	79.5	110	5	US-10-816-938-21
4	519	77.7	110	4	US-10-774-076-5
5	513	76.8	110	4	US-10-350-555-1
6	513	76.8	110	4	US-10-625-047-1
7	513	76.8	110	5	US-10-631-258-1
8	513	76.8	110	5	US-10-854-735-1
9	513	76.8	110	5	US-10-835-533-1
10	510	76.3	108	4	US-10-305-368-4
11	508	76.0	109	4	US-10-328-190-14
12	508	76.0	109	4	US-10-350-555-21
13	508	76.0	109	4	US-10-350-555-29
14	508	76.0	109	4	US-10-625-047-21
15	508	76.0	109	4	US-10-625-047-29
16	508	76.0	109	5	US-10-631-258-21
17	508	76.0	109	5	US-10-631-258-29
18	508	76.0	109	5	US-10-854-735-21
19	508	76.0	109	5	US-10-835-533-21
20	505	75.6	109	4	US-10-350-555-22
21	505	75.6	109	4	US-10-625-047-22
22	505	75.6	109	5	US-10-631-258-22
23	505	75.6	109	5	US-10-854-735-22
24	505	75.6	109	5	US-10-835-533-22
25	505	75.6	218	4	US-10-350-555-27
26	505	75.6	218	4	US-10-625-047-27
27	505	75.6	218	5	US-10-631-258-27

28	504	75.4	109	4	US-10-350-555-23	Sequence 23, Appl
29	504	75.4	109	4	US-10-625-047-23	Sequence 23, Appl
30	504	75.4	109	5	US-10-631-258-23	Sequence 23, Appl
31	504	75.4	109	5	US-10-854-735-23	Sequence 23, Appl
32	504	75.4	109	5	US-10-835-533-23	Sequence 23, Appl
33	504	75.4	218	4	US-10-350-555-28	Sequence 28, Appl
34	504	75.4	218	4	US-10-625-047-28	Sequence 28, Appl
35	504	75.4	218	5	US-10-631-258-28	Sequence 28, Appl
36	495.5	74.2	109	3	US-09-865-483-7	Sequence 28, Appl
37	495.5	74.2	109	4	US-10-726-555-7	Sequence 7, Appl
38	495	74.1	218	4	US-10-379-392-159	Sequence 159, App
39	490	73.4	109	4	US-09-940-727B-1	Sequence 1, Appl
40	486	72.8	107	4	US-10-328-180-10	Sequence 10, Appl
41	486	72.8	109	3	US-09-940-727B-2	Sequence 2, Appl
42	477	71.4	109	3	US-09-940-727B-3	Sequence 3, Appl
43	477	71.4	109	3	US-09-940-727B-121	Sequence 121, App
44	469	70.2	218	4	US-10-379-392-161	Sequence 161, App
45	460	68.9	218	4	US-10-379-392-164	Sequence 164, App

ALIGNMENTS

RESULT 1
US-10-768-193-8
Sequence 8, Application US/10768193
Publication No. US20040181042A1
GENERAL INFORMATION:
APPLICANT: MEDICAL & BIOLOGICAL LABORATORIES CO., LTD.
APPLICANT: The director of Chubu National Hospital
APPLICANT: YAMAGISAWA, Katsuhiko
APPLICANT: SHIBATA, Masao
TITLE OF INVENTION: Antibody recognizing GM1 ganglioside-bound
FILE REFERENCE: P0102402
CURRENT APPLICATION NUMBER: US/10/768, 193
CURRENT FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: JP P2001-235700
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: PCT/JP02/07874
PRIOR FILING DATE: 2002-08-01
NUMBER OF SEQ ID NOS: 16
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 129
TYPE: PRT
ORGANISM: Mus musculus
US-10-768-193-8

Query Match 100.0%; Score 668; DB 4; Length 129;
Best Local Similarity 100.0%; Pred. No. 2.8e-55;
Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAWTSILSLALCSGASSQAVVTOESALTSPGCVIILCRSGTAVTTSNTANVQEK 60
DB 1 MAWTSILSLALCSGASSQAVVTOESALTSPGCVIILCRSGTAVTTSNTANVQEK 60
QY PHLFTGLIGTSNRAPGVPRFSGSLIDGKALTTGAOTEDDAYFCALMSTHYVFG 120
DB 61 PHLFTGLIGTSNRAPGVPRFSGSLIDGKALTTGAOTEDDAYFCALMSTHYVFG 120
QY 121 GGTXTVTLG 129
DB 121 GGTXTVTLG 129

RESULT 2
US-10-816-938-8
Sequence 8, Application US/10816938
Publication No. US20040229301A1
GENERAL INFORMATION:
APPLICANT: Wang, Baiyang
TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof

FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 8
LENGTH: 112
TYPE: PRT
ORGANISM: Mus sp.
US-10-816-938-8

Query Match
Best Local Similarity 80.1%; Score 535; DB 5; Length 112;
Matches 101; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 20 QAVVQESALTTSPGGTIVLTCRSSGTAVTTSNYANWQEKPDHFTGLIGTSNRAPGV 79
DB 1 QAVVQESALTTSPGGTIVLTCRSSGTAVTTSNYANWQEKPDHFTGLIGTSNRAPGV 60
QY 80 PVRFGSLIGDKAALTTGAQTEDDAMFCAWSTHYVFGGKTVTVLG 129
DB 61 PARFSGSLIGDKAALTTGAQTEDEDAIFCALWSTHNVFGGGKTVTVLG 110

RESULT 3

US-10-816-938-21
Sequence 21, Application US/10816938
Publication No. US20040229301A1
GENERAL INFORMATION:
APPLICANT: Wang, Baiyang
TITLE OF INVENTION: Tissue Factor Antibodies and Uses Thereof
FILE REFERENCE: 1861.1670002
CURRENT APPLICATION NUMBER: US/10/816,938
CURRENT FILING DATE: 2004-04-05
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.2
SEQ ID NO 21
LENGTH: 110
TYPE: PRT
ORGANISM: Mus sp.
US-10-816-938-21

Query Match
Best Local Similarity 79.5%; Score 531; DB 5; Length 110;
Matches 100; Conservative 5; Mismatches 5; Indels 0; Gaps 0;

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QY 80 PVRFGSLIGDKAALTTGAQTEDDAMFCAWSTHYVFGGKTVTVLG 129
DB 61 PARFSGSLIGDKAALTTGAQTEDEDAIFCALWSTHNVFGGGKTVTVLG 110

RESULT 4

US-10-774-076-5
Sequence 5, Application US/10774076
Publication No. US20040210040A1
GENERAL INFORMATION:
APPLICANT: Protein Design Labs, Inc.
APPLICANT: Landolf, et al.
TITLE OF INVENTION: Amphipregulin Antibodies and Their Use to Treat Cancer and
FILE REFERENCE: 05882.0064.NPUS01
CURRENT APPLICATION NUMBER: US/10/774,076
CURRENT FILING DATE: 2004-02-06
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 110
TYPE: PRT
ORGANISM: mus sp.

US-10-774-076-5

Query Match
Best Local Similarity 77.7%; Score 519; DB 4; Length 110;
Matches 99; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

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DB 1 QAVVQESALTTSPGGTIVLTCRSSGTAVTTSNYANWQEKPDHFTGLIGTSNRAPGV 60
QY 80 PVRFGSLIGDKAALTTGAQTEDDAMFCAWSTHYVFGGKTVTVLG 129
DB 61 PARFSGSLIGDKAALTTGAQTEDEDAIFCALWSTHNVFGGGKTVTVLG 110

RESULT 5

US-10-350-555-1
Sequence 1, Application US/10350555
Publication No. US20040146934A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornillie, Todd
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-130900US
CURRENT APPLICATION NUMBER: US/10/350,555
CURRENT FILING DATE: 2003-01-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 110
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain
US-10-350-555-1

Query Match
Best Local Similarity 76.8%; Score 513; DB 4; Length 110;
Matches 96; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

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DB 1 QAVVQESALTTSPGGTIVLTCRSSGTAVTTSNYANWQEKPDHFTGLIGTSNRAPGV 60
QY 80 PVRFGSLIGDKAALTTGAQTEDDAMFCAWSTHYVFGGKTVTVLG 129
DB 61 PARFSGSLIGDKAALTTGAQTEDEDAIFCALWSTHNVFGGGKTVTVLG 110

RESULT 6

US-10-625-047-1
Sequence 1, Application US/10625047
Publication No. US20040198962A1
GENERAL INFORMATION:
APPLICANT: Meares, Claude
APPLICANT: Cornillie, Todd
TITLE OF INVENTION: The Regents of the University of California
FILE REFERENCE: 023070-130910US
CURRENT APPLICATION NUMBER: US/10/625,047
CURRENT FILING DATE: 2003-07-22
PRIOR APPLICATION NUMBER: US 10/350,555
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 110
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
OTHER INFORMATION: murine monoclonal antibody 2D12.5 light chain

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 21, 2006, 18:07:45 ; Search time 14.117 Seconds
(without alignments)
261.554 Million cell updates/sec

Title: US-10-768-193-8
Perfect score: 668
Sequence: 1 MATNTSLILSLALCSGASQ.....ALWSTHYVGGTKXTVLG 129

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 169630 seqs, 28622889 residues

Total number of hits satisfying chosen parameters: 169630

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	444.5	66.5	109	7	US-11-100-553B-37 Sequence 37, Appl
3	437.5	65.5	109	7	US-11-100-553B-36 Sequence 36, Appl
4	350	52.4	245	7	US-11-054-515-1523 Sequence 1523, Ap
5	329.5	49.3	240	7	US-11-000-463-248 Sequence 248, Ap
6	327.5	49.0	249	7	US-11-054-515-1838 Sequence 1838, Ap
7	323	48.4	108	7	US-11-064-174-51 Sequence 51, Appl
8	323	48.4	108	7	US-11-064-174-52 Sequence 52, Appl
9	321	48.1	108	7	US-11-064-174-166 Sequence 166, Appl
10	315.5	47.2	111	7	US-11-155-775-36 Sequence 890, Ap
11	312.5	46.8	251	7	US-11-054-515-890 Sequence 891, Ap
12	312.5	46.8	251	7	US-11-054-515-891 Sequence 894, Ap
13	312.5	46.8	251	7	US-11-054-515-894 Sequence 903, Ap
14	312.5	46.8	251	7	US-11-054-515-903 Sequence 910, Ap
15	312.5	46.8	251	7	US-11-054-515-1121 Sequence 1121, Ap
16	312.5	46.8	251	7	US-11-054-515-1126 Sequence 1140, Ap
17	312.5	46.8	251	7	US-11-054-515-1140 Sequence 1141, Ap
18	312.5	46.8	251	7	US-11-054-515-1141 Sequence 1147, Ap
19	312.5	46.8	251	7	US-11-054-515-1147 Sequence 1148, Ap
20	312.5	46.8	251	7	US-11-054-515-1148 Sequence 1157, Ap
21	312.5	46.8	251	7	US-11-054-515-1157 Sequence 1162, Ap
22	312.5	46.8	251	7	US-11-054-515-1162 Sequence 1173, Ap
23	312.5	46.8	251	7	US-11-054-515-1173 Sequence 1173, Ap
24	312.5	46.8	251	7	US-11-054-515-1173 Sequence 1173, Ap
25	311	46.6	119	7	US-11-000-463-720 Sequence 720, Ap

26	309.5	46.3	251	7	US-11-054-515-1127 Sequence 1127, Ap
27	307	46.0	108	7	US-11-064-174-53 Sequence 53, Appl
28	305.5	45.7	251	7	US-11-054-515-1151 Sequence 1151, Ap
29	301.5	45.1	251	7	US-11-054-515-1166 Sequence 1166, Ap
30	296.5	44.4	251	7	US-11-054-515-1152 Sequence 1152, Ap
31	291	43.6	98	7	US-11-084-554-219 Sequence 219, Ap
32	291	43.6	98	7	US-11-136-250-219 Sequence 220, Ap
33	287	43.0	98	7	US-11-084-554-220 Sequence 220, Ap
34	287	43.0	98	7	US-11-136-250-220 Sequence 220, Ap
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36	275.5	41.2	253	7	US-11-054-515-1938 Sequence 1938, Ap
37	270	40.4	232	7	US-11-000-463-343 Sequence 343, Ap
38	267.5	40.0	231	7	US-11-000-463-283 Sequence 283, Ap
39	265.5	39.7	249	7	US-11-054-515-1312 Sequence 1312, Ap
40	264.5	39.6	244	7	US-11-054-515-1842 Sequence 1842, Ap
41	264	39.5	99	7	US-11-084-554-221 Sequence 221, Ap
42	264	39.5	99	7	US-11-136-250-221 Sequence 221, Ap
43	261	39.1	253	7	US-11-054-515-1364 Sequence 1364, Ap
44	259	38.8	236	7	US-11-000-463-815 Sequence 815, Ap
45	255	38.2	245	7	US-11-054-515-1864 Sequence 1864, Ap

ALIGNMENTS

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RESULT 1
US-10-726-554-7
Sequence 7, Application US/10726554
Publication No. US20050249753A1
GENERAL INFORMATION:
APPLICANT: LEE, Jong Wook et al.
TITLE OF INVENTION: A VARIABLE REGION OF THE MONOCLONAL ANTIBODY AGAINST
THE HBV S-SURFACE
TITLE OF INVENTION: THE HBV S-SURFACE
FILE REFERENCE: 1599-0197P
CURRENT APPLICATION NUMBER: US/10/726,554
CURRENT FILING DATE: 2003-12-04
PRIOR APPLICATION NUMBER: US/09/865,483
PRIOR FILING DATE: PRIORITY FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
LENGTH: 109
TYPE: PRT
ORGANISM: Escherichia coli
US-10-726-554-7

Query Match      74.2% Score 495.5; DB 6; Length 109;
Best Local Similarity 85.5%; Pred. No. 1.5e-35;
Matches 94; Conservative 10; Mismatches 5; Indels 1; Gaps 1;

Cy      20 QAVVQESALITSPGTVILTCRSSSTGAVTTSYANVVOEKPDHIFTGLIGTSNRAAPGV 79
      1 QAVVQESALITSPGTVILTCRSSSTGAVTTSYANVVOEKPDHIFTGLIGTSNRAAPGV 60
      61 PAFVSGSLIDKXALITTGATDEDAIFCALWYN-NWVFGGGTKXTVLG 109

Db      80 PAFVSGSLIDKXALITTGATDEDAIFCALWYN-NWVFGGGTKXTVLG 129
      61 PAFVSGSLIDKXALITTGATDEDAIFCALWYN-NWVFGGGTKXTVLG 109

RESULT 2
US-11-100-553B-37
Sequence 37, Application US/11100553B
Publication No. US20060014937A1
GENERAL INFORMATION:
APPLICANT: HENI II, KANG, et al.
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
FILE REFERENCE: Q87350
CURRENT APPLICATION NUMBER: US/11/100,553B
CURRENT FILING DATE: 2005-04-07
PRIOR APPLICATION NUMBER: KR10-2004-25573
PRIOR FILING DATE: 2004-04-14
NUMBER OF SEQ ID NOS: 43
```

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; SOFTWARE: Koparentin 1.71
; SEQ ID NO 37
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized light chain LFW22-312
US-11-100-553B-37

Query Match
Best Local Similarity 76.4%; Pred. No. 36-31;
Matches 84; Conservative 12; Mismatches 13; Indels 1; Gaps 1;

OY 20 QAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNRAGV 79
Db 1 QAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNRAGV 60

OY 80 PVRFSGSLIGDKAALITGAGTDEDDAMVFCALMYSTHYVFGGKTVTVLG 129
Db 61 PARFSGSLIGDKAALITGAGTDEDDAMVFCALMYN-NMVFSGGKTVTVLG 109

RESULT 3
US-11-100-553B-36
; Sequence 36, Application US/11100553B
; Publication No. US20060014937A1
; GENERAL INFORMATION:
; APPLICANT: Heul 11, KANG, et al.
; TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST S-SURFACE ANTIGEN OF HEPATITIS B VIRUS
; FILE REFERENCE: 087350
; CURRENT APPLICATION NUMBER: US/11/100,553B
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: KR10-2004-25573
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: Koparentin 1.71
; SEQ ID NO 36
; LENGTH: 109
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variable region of humanized light chain LFW22-31
US-11-100-553B-36

Query Match
Best Local Similarity 74.5%; Pred. No. 1-26-30;
Matches 82; Conservative 14; Mismatches 13; Indels 1; Gaps 1;

OY 20 QAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNRAGV 79
Db 1 QAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNRAGV 60

OY 80 PVRFSGSLIGDKAALITGAGTDEDDAMVFCALMYSTHYVFGGKTVTVLG 129
Db 61 PARFSGSLIGDKAALITGAGTDEDDAMVFCALMYN-NMVFSGGKTVTVLG 109

RESULT 4
US-11-054-515-1523
; Sequence 1523, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind H1ys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
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; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1523
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-1523

Query Match
Best Local Similarity 60.3%; Pred. No. 6-5e-23;
Matches 70; Conservative 13; Mismatches 31; Indels 2; Gaps 1;

OY 16 GASSQAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNR 75
Db 130 GGSQAVVQESALITTSPCGTIVLTICRSSTGAVTTSNYANWQEKPDHLFTGLIGTSNR 189

OY 76 APGVPRFSGSLIGDKAALITGAGTDEDDAMVFCALMY--STHYVFGGKTVTVLG 129
Db 190 HSWTPARFSGSLIGDKAALITGAGTDEDDAMVFCALMYN-NMVFSGGKTVTVLG 245

RESULT 5
US-11-000-463-248
; Sequence 248, Application US/11000463
; Publication No. US20050266423A1
; GENERAL INFORMATION:
; APPLICANT: Tang, Y Tom
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Chen, Rui-hong B.
; APPLICANT: Qian, Xiaohong B.
; APPLICANT: Wang, Zhiwei
; APPLICANT: Wehrman, Tom
; APPLICANT: Zhang, Jie
; APPLICANT: Zhou, Ping
; APPLICANT: Cao, Yi-Cheng
; APPLICANT: Drmanac, Radoje T.
; TITLE OF INVENTION: Novel Nucleic Acids and Polypeptides
; FILE REFERENCE: 785CIP4CN
; CURRENT APPLICATION NUMBER: US/11/000,463
; CURRENT FILING DATE: 2004-11-28
; PRIOR APPLICATION NUMBER: 10/291,265
; PRIOR FILING DATE: 2002-11-08
; PRIOR APPLICATION NUMBER: PCT/US01/02623
; PRIOR FILING DATE: 2001-01-25
; PRIOR APPLICATION NUMBER: 09/922,279
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 248
; LENGTH: 240
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